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152102

From: Slobodyansky, Elizabeth
Sent: Friday, April 29, 2005 2:53 PM
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Subject: 08/952,741 SEQ

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Please search for case 08/952,741:

es

SEQ ID NOs: 1 and 2 against commercial and ~~interference~~ databases.

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Elizabeth Slobodyansky, PhD

Primary Examiner
Art Unit 1652
REM 2D83
571-272-0941
MAILBOX 2C70

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Searcher: _____
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Date Searcher Picked up: _____
Date Completed: _____
Searcher Prep/Rev. Time: _____
Online Time: _____

Type of Search

NA#: _____ AA#: _____
Interference: _____ SPDI: _____
S/L: _____ Oligomer: _____
Encode/Transl: _____
Structure#: _____ Text: _____
Inventor: _____ Litigation: _____

Vendors and cost where applicable

STN: _____
DIALOG: _____
QUESTEL/ORBIT: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: _____
WWW/Internet: _____
Other(Specify): _____

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Best Local Similarity 100.0%; Pred. No. 0;
Matches 1776; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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LOCUS AR411953
DEFINITION Sequence 1 from patent US 6638748.
ACCESSION AR411953
VERSION AR411953.1 GI:40164465
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

Unclassified.

1 (bases 1 to 1776)

AUTHORS Hatada, Y., Ozaki, K., Ara, K., Kawai, S. and Ito, S.

TITLE Gene encoding alkaline lipolytic alpha-amylase

JOURNAL Patent: US 6638748-A 1 28-OCT-2003;

FEATURES Location/Qualifiers

source

1. 1776

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ORIGIN

Query Match 100.0%; Score 1776; DB 6; Length 1776;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1776; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 ATATTAATTTGAAATGAACCTTATGAAATATGATGCGGACGAGAAAAAC 60
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REFERENCE      1
AUTHORS        Andersen, C.
TITLE          Alpha-amylase variant with altered properties
JOURNAL        Patent: WO 0231124-A 7 18-APR-2002;
               Novozymes A/S (DK)
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 1776; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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VERSION AB008763.1 GI:3445479
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SOURCE Bacillus sp.
ORGANISM Bacillus sp.
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AUTHORS Igarashi, K., Hatada, Y., Ikawa, K., Araki, H., Ozawa, T., Kobayashi, T., Ozaki, K. and Ito, S.
TITLE Improved thermostability of a Bacillus alpha-amylase by deletion of an arginine-glycine residue is caused by enhanced calcium binding
JOURNAL Biochem. Biophys. Res. Commun. 248 (2), 372-377 (1998)
MEDLINE 98342096
PUBMED 9675143
REFERENCE 2 (bases 1 to 1786)
AUTHORS Hatada, Y.
TITLE Direct Submission
JOURNAL Submitted (10-NOV-1997) Yuji Hatada, Kao Corporation, Tochigi Research Laboratories, 2606 Akabane, Ichikai, Haga-gun, Tochigi 321-3497, Japan (tel:0285-68-7400, fax:0285-68-7403)
LOCATION/Qualifiers

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ORIGIN
Query Match 100.0%; Score 1776; DB 1; Length 1786;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1776; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 DEFINITION Variant alpha-amylase.
 ACCESSION E51838
 VERSION E51838.1 GI:18629544
 KEYWORDS JP 2000245466-A/1.
 SOURCE unidentified
 ORGANISM unidentified.
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 REFERENCE 1 (bases 1 to 1786)
 AUTHORS Igarashi, K., Endo, K., Hayashi, Y., Hagiwara, H. and Oz, K.
 TITLE Variant alpha-amylase
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 PN JP 2000245466-A/1
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Query Match 100.0%; Score 1776; DB 6; Length 1786;
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DEFINITION Sequence 1 from patent US 6743616.
ACCESSION ARS41695
VERSION ARS41695.1 GI:53933768
KEYWORDS
SOURCE
ORGANISM
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AUTHORS Araki, H., Endo, K., Hagihara, H., Igarashi, K., Hayashi, Y. and Ozaki, K.
TITLE Highly productive alpha-amylases
JOURNAL Patent: US 6743616-A 1 01-JUN-2004;
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Query Match 100.0%; Score 1776; DB 6; Length 1786;
Best Local Similarity 100.0%; Pred. No. 0; Mismatches 0; Indels 0; Gaps 0;
Matches 1776; Conservative 0;

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DEFINITION Sequence 3 from Patent EP1199336.
ACCESSION AX428291
VERSION AX428291.1 GI:21538247
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Bacillus sp. KSM-Ap1378
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
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1 Areki, H.C., Hagihara, H.C., Hayashi, Y.C., Endo, K.C., Igarashi, K.C.
and Ozaki, K.C.
Highly productive alpha-amylases
Patent: EP 1199356-A 3 24-APR-2002;
Kao Corporation (JP)
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Db 1091 ACAAGTTGAGATACCTCCGTTGCAATGCTCTCATTAATTTGTAATGATGATGATGAT 1150
QY 1141 AATAGTGTGCTATTTGATATGAGAAATATTTAAATGTTCTGCTGTAACAAAACAC 1200
Db 1151 AATAGTGTGCTATTTGATATGAGAAATATTTAAATGTTCTGCTGTAACAAAACAC 1210
QY 1201 CCTATACATGACATCAATTTGTTGATTAACATGACTCTCAGCAGAGAAAGCATTTGAA 1260
Db 1211 CCTATACATGACATCAATTTGTTGATTAACATGACTCTCAGCAGAGAAAGCATTTGAA 1270
QY 1261 TCCCTTTGTCATCGGTGTTCAACACATGCGCATATGATGATTTGCAAGGGAGCAA 1320
Db 1271 TCCCTTTGTCATCGGTGTTCAACACATGCGCATATGATGATTTGCAAGGGAGCAA 1330
QY 1321 GGTTAACCTTCCGTATTTTACGGTGTATTAACGGTATACCAATGATGTTCTCTTG 1380
Db 1331 GGTTAACCTTCCGTATTTTACGGTGTATTAACGGTATACCAATGATGTTCTCTTG 1390
QY 1381 ATGAATATCTAAATTTGATCACTTGTGAGGACGTCAAACGATATCTTAACGAAACCAA 1440
Db 1391 ATGAATATCTAAATTTGATCACTTGTGAGGACGTCAAACGATATCTTAACGAAACCAA 1450
QY 1441 CATGATATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1500
Db 1451 CATGATATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1510

QY 1501 CCAATTCAGACTTGCACATATATATGTCGATGGGCCAGGGGATTAATATGATGAT 1560
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QY 1561 GTGCGGAAACATTAAGCTGGCCAGATATGAGAGATATCACCGGAATATGCTGTGATCC 1620
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QY 1621 GTACACATTAATGCAAGATGTTGGGGAAATTTCACTGTATTAAGGAGGGGCACTTCCGTT 1680
Db 1631 GTACACATTAATGCAAGATGTTGGGGAAATTTCACTGTATTAAGGAGGGGCACTTCCGTT 1690
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Db 1751 CCGATCACTCATACACCCATTAATTAATTTGGAAGCTT 1786

RESULT 9
AX601433/c 6661 bp DNA linear PAT 17-FEB-2003

LOCUS AX601433 Sequence 3 from Patent WO02092741.
DEFINITION AX601433
ACCESSION AX601433
VERSION AX601433.1 GI:28401480

KEYWORDS
SOURCE
ORGANISM
synthetic construct
synthetic construct
other sequences; artificial sequences.

REFERENCE
AUTHORS
TITLE
JOURNAL
1
EskeJund,M.B., Schuelein,M., Nielsen,V.S. and Smeets,J.
Detergent compositions comprising Bacillus subtilis pectate lyases
Patent: WO 02092741-A 3 21-NOV-2002;
Novozymes A/S (DK)

FEATURES
source
1..6661
Location/Qualifiers
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Plasmid pMOD995"

ORIGIN
Query Match
Best Local Similarity 84.1%; Pred. No. 1.9e-267;
Matches 1339; Conservative 0; Mismatches 253; Indels 0; Gaps 0;

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Db 3882 AGAAATGAGAGGAGAGAAACATGATTCAAAACGAAAGCGGACAGTTTGTTCAGAC 3823
QY 179 TAACTATTTGTAGCTGTAGCTGTTTGTTCATATATGACGAAACAGACAAAGCCC 238
Db 3822 TTGTGCTTATATGCAACGCTGTTATTTGTCAAGTTTCCGATTAACAAAACATCGCGGCC 3763
QY 239 ATCATTAATGAGAGATGGGACCATATGATGACATTTTGAATGATGATTTGCCAATGACG 298
Db 3762 ATCATTAATGAGAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3703
QY 299 GGAACCACTGAAACAGGTTACAGATGACGACGCTTAATTAAGATTAAGGATTAACCG 358
Db 3702 GGAATCATTTGAAACAGGTTGAGAGATGACGACGCTTAATTAAGATTAAGGATTAACCG 3643
QY 359 CTGTTTGAATTTCTCTGATGAGAGGGGACTTCCGAAATATATGATGATGATGATGAT 418
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QY 419 ATGATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 478
Db 3582 ATGATTTATATATATCTTGGAGAGTTTAAACAGAGAGGAGGATTTGTATACAAATATGAA 3523
QY 479 CAAGAGTCAGTTGCAAGGTGCGGTGACATCTTTGAAAAATTAACGGGATTCAGATTATG 538

D	b		3522	CACGCACCAAGCTACAGGCTGGCGGTGACCTCTTTAAATAATACGGCATTTCAGGTATATG	3465
O	y		539	GGGATGTCGTGATGATCATTAAGGTGAGCGACGAGCAGAGATGTTAAATGGCGTGG	598
D	b		3462	GTGATGTGCTCATGATCATTAAGGTGAGCGATGTGATCGGAATTTGTTAAATGGCGTGG	3403
O	y		559	AAGTGAACCGAAGCAACCGAAACCAAGAAATTCAGGTGATATCACATTTGAAGCATGGA	658
D	b		3402	AAGTGAATCGAGCAACCGAAACCAAGAAACCTCAGAGAGATATCAATAGAAAGGTGGA	3343
O	y		659	CGAAATTTGATTTCCCTGGAGAGAGAAATACCATTCCAACTTTAAATGGCGCTGTATC	718
D	b		3342	CAAAAGTTGATTTTCTGGAAAGGAATTAACCATTTCCAGCTTTAAAGTGGCGCTGTATC	3283
O	y		719	ATTTTGATGGGACAGATTGGGATCACTCACTCACTTCAGAACAAATATATAAATTC	778
D	b		3282	ATTTTGATGGGACAGATTGGGATCACTCACTCACTTCAGAACAAATATATAAATTC	3222
O	y		779	GAGGTACCGGAAAGGCATGGGACTGGGAAATGATATAGAAACGGCAACTATGATTAAC	838
D	b		3222	GGGGAAACGGCAAGGCTGGGACTGGGAAATGATATAGAAACGGCAACTATGATTAAC	3163
O	y		839	TTATGATACCAACATTTGATATGATATCACTCCAGATATATCAATGAATTTGAATTTGG	898
D	b		3162	TTATGATACCAACCGGTATGATATCACTCCAGAGTATATCATGAATTTGAATACTGGG	3103
O	y		899	GAGTTTGGTATCAAAATACCTTAATCTGATGATGATTTGAATTCAGTCTGTGAACATA	958
D	b		3102	GAGTGTGGTATCAAAATACCTTAATCTGATGATGATTTGAATTCAGTCTGTGAACATA	3043
O	y		959	TTAAATACAGCTATACGAGAGATTGGCTTAACAATGTGCTGAACCAACAGGTAAACCA	1018
D	b		3042	TAAATATATAGCTTTACGAGAGATTGGCTTAACAATGTGCTGAACCAACAGGTAAACCA	2983
O	y		1019	TGTTTGCACTTGCAGAAATTTTGGAAAAATGACCTTGCTGCAATCGAAAACTATTTAATA	1078
D	b		2982	TGTTTGCACTTGCAGAAATTTTGGAAAAATGACCTTGCTGCAATTTGAATA	2923
O	y		1079	AAACAAGTTGGAATCACTCCGTGTCGATGTCCTCTTCATATATATTTGTAACAATGAT	1138
D	b		2922	AAACAAGTTGGAATCACTCCGTGTCGATGTCCTCTCTCACTATATTTGTAACAATGAT	2863
O	y		1139	CTAATAGTGTGGCTAATTTTGTATGAGAAATATTTAAATGTTCTGTGTAACAAAAC	1198
D	b		2862	CTAATAGTGTGGCTAATTTTGTATGAGAAATATTTAAATGTTCTGTGTAACAAAAC	2803
O	y		1199	ACCTATATACATGACATCACTTTGTTGATTAACATGACCTCTACGCAGAGAAAGCATGG	1258
D	b		2802	ATCCCAACATCCCGTACTTTTGTGTTATMACATGATTTCTACGCCGGGAAAGCATGG	2743
O	y		1259	AATCCTTTGTTGAATCGTGTGTAACAACCACTGGCATATGATGATTTGTAACAAGGAGC	1318
D	b		2742	AATCCTTTGTTGAATCGTGTGTAACAACCACTGGCATATGATGATTTGTAACAAGGAGC	2683
O	y		1319	AAGGTACCCCTTCGATTTTAAACGATGATTACTACGATTAACCAACTATGTTCTCTT	1378
D	b		2682	AAGGTATACCTTCGATTTTAAACGATGATTACTACGATTAACCAACTATGTTCTCTT	2623
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D	b		2622	CTATGAATCTTAAATTTGATTCATTTCTGACAGGACGTCMAACGATATGCTTACGGAACC	2563
O	y		1439	AACATGATTAATTTGATATCATGATATTAATGCGCTGGAACGAGAAAGGAGAAATGCTCC	1498
D	b		2562	AACATGATTAATTTGATATCATGATATTAATGCGCTGGAACGAGAAAGGAGAAATGCTCC	2503
O	y		1499	ACCCAAATTCAGAGCTTGCMACTATATATGTCGATGGGACAGGGGGTATATAATGATATG	1558
D	b		2502	ATCCAAATTCAGAGCTTGCMACTATATATGTCGATGGGACAGGGGGTATATAATGATATG	2443
O	y		1559	ATGTGGGAAACATTAAGCTGGCCAAATGATGAGATATCAACGGAAATAGTCTGTGTA	1618

QY	Db	2442	ATGTGGGGAAAAAATTAACCGGGACAAGTTTGGAGAGATATTACCGGAAATAGCACAGCA	2383
QY	1619	CCGTCACCATTAATGCAGATGGTGGGGAAATTTCACTGTAAACGGAGGSCAGATTTCCG	1678	
Db	2382	CCGTCACAATTAATGCACAGCGAGTGGGGTAAATTTCTCTGTAAATGAGAGGTCCTGTTCCG	2323	
QY	1679	TTTGGGTGAACCAATTAATTAAGAACCAAGAG	1710	
Db	2322	TTTGGGTGAACCAATTAAGGTTTGATTAAGAG	2291	
RESULT 10				
LOCUS	AR087556	1458 bp	DNA	linear
DEFINITION	Sequence 11 from patent US 5989169.			
ACCESSION	AR087556			
VERSION	AR087556.1	GI:10014319		
KEYWORDS				
SOURCE	Unknown.			
ORGANISM	Unknown.			
REFERENCE	Unclassified.			
AUTHORS	1 (bases 1 to 1458)			
TITLE	Swendsen A., Biesg. ang. rd-Frantzen, H. and Borchert, T. Vedel.			
JOURNAL	.alpha.-amylase mutants			
FEATURES	Patent: US 5989169-A 11 23-NOV-1999;			
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ORIGIN	/mol_type="unassigned DNA"			
Query Match				
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	Matches 1278; Conservative	0; Mismatches 180; Indels 0; Gaps 0;		
QY	238	CATCATATGGAGCAATGGGACCATGATGAGATTTTGAATGGCATTTGCCAAATGAC	297	
Db	1	CATCATATGGACAAATGAGTACTATGATGCAATATTTGCATGGTATTTGCCAAATGAC	60	
QY	298	GGGAACCACTGGAACAGGTTACGAGATGACGACGCTAACCTTAAAGATGAAAGGATTC	357	
Db	61	GGGAATCATTTGGAACAGGTTAGGGATGACGACGCTAACCTTAAAGATGAAAGGATTAACA	120	
QY	358	GCTGTTTGGATTCCTCCTGCATGGAAGGGGACTTCGCAAAATGATGTTGGGTATGCTCC	417	
Db	121	GCTGATGATGATCCACCTGCATGGAAGGGGACTTCGCAATGATGATGTTATGGAAGCC	180	
QY	418	TATGATTTTGAACGATCTTGATGAGTTTAAACCAAAAGGAAACCGTCCTGTAACAAATATGCG	477	
Db	181	TATGATTTTATATGATCTTGGAGAGTTTAAACGAAAGGGGACGGTTCGTACAAATATATGGA	240	
QY	478	ACAAGGATGAGTTGGCAAGTGCCTGATCATCTTTGAAAATTAACGGGATTCAGATTTAT	537	
Db	241	ACAACGCAACAGCTACAGGCTGCGGTGATCTCTTTAAAAATTAACGGCATTCAGGATATAT	300	
QY	538	GGGATGTCGTATGATGATCATTAAGAGTGTGACAGACGGGACAGAGATGTTAAATGCGGTG	597	
Db	301	GGTATATGTCGTATGATGATCATTAAGAGTGTGACAGAGATGTTAGAAATTTGTAAATGCGGTA	360	
QY	598	GAAATGAAACGAAACCGAAACCAAGAAATATCAGGTGATACACCATTTGAAGCATGG	657	
Db	361	GAAATGAAACCGAGCAACCGAAACCAAGAAACCTCAGAGAGATATGCAATGAAAGCGTGG	420	
QY	658	ACGAAATTTGATTTCCCTGGAAAGGAAATATCCATTCGAACTTTAAATGGCGCGTGTAT	717	
Db	421	ACAAAGTTGATTTTCTCGGAAAGGAAATATCACTTCCAGCTTTAAGTGCGCTGGAT	480	
QY	718	CATTTTATGAGACAGATTTGGATCAGTCAGTCAGCTTCAGAACAAATATATAATTC	777	
Db	481	CATTTTATGAGACAGATTTGGATCAGTCAGTCAGCTTCAGAACAAATATATAATTC	540	
QY	778	AGAGTACCGGAAAGGCATGGGACTGGGAAATGATATATAGAAACGCACTATGATTAAC	837	

Db 541 AGGGGAACGAGAGCGCTGGGACTGGGAGTGCATACAGAGATGGCAACTATGACTAT 600
QY 838 CTTATGTATGACAGACATTGATATGATCATCCGAGAGTAATCAATGAACCTTAGAAATTGG 897
Db 601 CTTATGTATGACAGACCGTATGATGATCAACCCGAGAGTAATCAATGAACCTTAGAAATTGG 660
QY 898 GAGGTTGGTATCAAAATCACTTAATCTAGATGAGATTAGATGCATGCTGGAACAT 957
Db 661 GAGGTTGGTATCAAAATCACTTAATCTAGATGAGATTAGATGCATGCTGGAACAT 720
QY 958 ATTAATATACAGTATACAGAGATGGCTTAACATATGCTGTAACCAACAGGTAAACCA 1017
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QY 1138 TCTAATATGTTGGTGAATTTTGTATGAGAAATATTTTAAATGTTCTGTCTGTACAAAA 1197
Db 901 TCTAATATGCGTGTATTTATGATATGAGAAATATTTTAAATGTTCTGTGTGTGCAAAAA 960
QY 1198 CACCTTATACATGACATGATGTTGATTAACCATGATCTCTGACCGAGAGACATG 1257
Db 961 CACCTTATACATGACATGTTGTTGTTGATTAACCATGATCTCTGACCGAGAGACATG 1020
QY 1258 GAATCCCTTGTGAATGCTGTTCAACCACTGCGCATATGATGATTTCTGACAGAGGAG 1317
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QY 1318 CAAAGTTACCTTCCGTAATTTTACGATGATTAACGATTAACCACTGATGTTCTT 1377
Db 1081 CAAAGTTATCTTCCGTAATTTTATGAGGATTAACGATTAACCACTGATGTTCTTCCG 1140
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QY 1438 CAAATGATATTTTGTATCATCATGATATATGCGCTGACAGAGAGAGGAGCAGCTCC 1497
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Db 1261 CACCAATTTTCAAGGCTTGGCACTATTTATGTCGATGAGGCGAGGCGGTAATTAATGATG 1320
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QY 1618 ACCGTCAACATTAATGAGATGTTGGGGAATTTCTGTAACCGAGGAGGAGGAGTTTTCG 1677
Db 1381 ACCGTCAACATTAATGAGAGATGTTGGGGAATTTCTCTGTATAGAGGAGTCCGTTTTCG 1440
QY 1678 GTTTGGGTGAAGCAATTA 1695
Db 1441 GTTTGGGTGAAGCAATTA 1458

RESULT 11
AR224266

LOCUS AR224266 1458 bp DNA linear PAT 26-SEP-2002
DEFINITION Sequence 11 from patent US 6440716.

ACCESSION AR224266
VERSION AR224266.1 GI:23333033

KEYWORDS

SOURCE Unknown.
ORGANISM Unknown.
Unclassified.

4

REFERENCE 1 (bases 1 to 1458)
AUTHORS Svendsen,A., Bisgard-Frantzen,H. and Borchert,T.V.
TITLE .alpha.-amylase mutants
JOURNAL Patent: US 6440716-A 11 27-AUG-2002;
FEATURES
source Location/Qualifiers
1..1458
/organism="unknown"
/mol_type="genomic DNA"
ORIGIN
Query Match 65.9%; Score 1170; DB 6; Length 1458;
Best Local Similarity 87.7%; Pred. No. 2,4e-263;
Matches 1278; Conservative 0; Mismatches 180; Indels 0; Gaps 0;
QY 238 CATCATTAATGGGACCAATGGGACCATGATGACGATATTTGATGGATTTGGCAATGAC 297
Db 1 CATCATTAATGGGACCAATGGGACTATGATGACATATTTGAAATGATTTGGCAATGAC 60
QY 298 GGGAAACCATGGAAACAGTTACGAGATGACGAGCTTAACCTTAAGAGTAAAGGATTAAC 357
Db 61 GGGAAATCATTTGAAACAGTTGAGGATGACGAGCTTAACCTTAAGAGTAAAGGATTAAC 120
QY 358 GCTGTTGGATTCCTCTGATGATGAAAGGAGCTTGCAGAAATGATGTTGGTATGCTGCC 417
Db 121 GCTGATGATCCACCTGATGAAAGGAGCTTCCAGAAATGATGATGATGAGAGCC 180
QY 418 TATGATTTGTAGATCTTGTGATTTAACCAGAAAGGAAACCGTCCGTACAAATATGAGC 477
Db 181 TATGATTTATGATCTTGTGAGATTTAACCAGAAAGGAGGAGGATGTAACAAATATGGA 240
QY 478 ACAAGAGTCAAGTTGCAAGTCCCGTCAATCTTTGAAATTAACGAGATTCAGTTTAT 537
Db 241 ACAAGAACCAAGCTACAGCTCGGATCTCTTTAAATTAACGAGATTCAGGATATAT 300
QY 538 GGGAGTGTGTATGATATTAAGGTGAGACAGCGGACAGATGATGTTAAATGCGGTG 597
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QY 598 GAAGTGAACCGAAACGAAACGAAATTAACGAGTAAATCACTTGAAGCATG 657
Db 361 GAAGTGAACCGAGCAACGAAACGAAACCTCAGAGATGATGATGATGATGATGATGATG 420
QY 658 ACGAAATTTGATTTCCCTGGAAGAGAGAAATACCAATCCATTTTAAATGAGCGCTGAT 717
Db 421 ACGAAATTTGATTTCCCTGGAAGAGAGAAATTAACATTCAGCTTAAATGAGCGCTGAT 480
QY 718 CATTTGATGGAACAGATTTGGATCACTGACCTTCAAGACAAATATTAATTC 777
Db 481 CATTTGATGGAACAGATTTGGATCACTGACCTTCAAGACAAATATTAATTC 540
QY 778 AAGAGTACCGGAAGGACATGGGACCTGGGAAGTATATGAGAGGCGCAACTATGATAC 837
Db 541 AAGGGAACAGGCAAGGCTGGGACCTGGGAAGTATATGAGAGAGTATGCACTATGACTAT 600
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 QY 1618 ACCGTACCATTAATGATGATGATGATGATGATGATGATGATGATGATGATG 1677
 Db 1381 ACCGTACCATTAATGATGATGATGATGATGATGATGATGATGATGATGATG 1440
 QY 1678 GTTGGTGGAAGCAATTA 1695
 Db 1441 GTTGGTGGAAGCAATTA 1458

RESULT 12
 LOCUS AR027254 1455 bp DNA linear PAT 29-SEP-1999
 DEFINITION Sequence 4 from patent US 5856164.
 ACCESSION AR027254
 VERSION AR027254.1 GI:5938094
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 UNCLASSIFIED.

REFERENCE 1 (bases 1 to 1455)
 AUTHORS Oultrud,H., Bisg,ang,rd-Franzen,H., stergaard,P., Rahbek,.,
 Rasmussen,M.,dolberg, and Van Der Zee,P.,
 TITLE Alkaline bacillus amylose
 JOURNAL Patent: US 5856164-A 4 05-JAN-1999;
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ORIGIN

Query Match 65.7%; Score 1167; DB 6; Length 1455;
 Best Local Similarity 87.6%; Pred.No. 1.2e-267;
 Matches 1275; Conservative 0; Mismatches 180; Indels 0; Gaps 0;
 QY 238 CATATATGGAAGGATGGAAGGATGGAAGGATGGAAGGATGGAAGGATGGAAGG 297
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 QY 298 GGAAGCACTGGAAGGATGGAAGGATGGAAGGATGGAAGGATGGAAGGATGGAAG 357
 Db 1 GGAAGCACTGGAAGGATGGAAGGATGGAAGGATGGAAGGATGGAAGGATGGAAG 1200

Db 61 GGAAGCACTGGAAGGATGGAAGGATGGAAGGATGGAAGGATGGAAGGATGGAAG 120
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 QY 418 TATGATTTATATGATCTTGGATGATGATGATGATGATGATGATGATGATGATGATG 477
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 Db 361 GAAGTGAACCGAAGCAACCGAAGCAACCGAAGCAACCGAAGCAACCGAAGCAAC 420
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RESULT 13
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LOCUS AR049517
DEFINITION Sequence 4 from patent US 5824531.
ACCESSION AR049517
VERSION AR049517.1 GI:6005556
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1455)
AUTHORS Outtup,H., Bleg.ang. rd-Frantzen,H., stergaard,P.Rahbek.,
Rasmussen,M.Dolberg. and Van der Zee,P.
TITLE Alkaline bacillus amylose
JOURNAL Patent: US 5824531-A 4 20-OCT-1998;
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Best Local Similarity 87.6%; Pred. No. 1,2e-262;
Matches 1275; Conservative 0; Mismatches 180; Indels 0; Gaps 0;
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QY 358 GCGTGTGATTCCTCTGATGAGAGGGAATTCGCCAAATGATGTTGGTATGAGTGC 417
Db 121 GCGTGTGATTCCTCTGATGAGAGGGAATTCGCCAAATGATGTTGGTATGAGTGC 180
QY 418 TATGATTTGATGATCTTGTGAGTTTAACCAAAAGGGAACCGTCCGTACAAATATGAGC 477
Db 181 TATGATTTGATGATCTTGTGAGTTTAACCAAAAGGGAACCGTCCGTACAAATATGAGC 240
QY 478 ACAAGAGATCAGTTGCAAGGTGCGCGTGAATCTTTGAAATTAACGGGATTCAGTTTAT 537
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QY 538 GGGGATGTCGTGATGATCATTAAGGTGAGAGACAGGGGACAGAGATGTAATGCGGTG 597
Db 301 GGGGATGTCGTGATGATCATTAAGGTGAGAGACAGGGGACAGAGATGTAATGCGGTG 360
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Db 1381 ACCGTACCATTTATTCAGAGCGATGGGGTATTTCTCTGTATATGAGGGGTCGTTTGG 1440
QY 1678 GTTTGGGTGAAGCAA 1692
Db 1441 GTTTGGGTGAAGCAA 1455

RESULT 14
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DEFINITION Sequence 4 from patent US 6093562.
ACCESSION ARI04348
VERSION ARI04348.1 GI:12817056
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1455)
AUTHORS Bisg ang.rd-Frantzen,H., Svendsen,A. and Borchert,T.Vedel.
TITLE Amylase variants
JOURNAL Patent: US 6093562-A 4 25-JUL-2000;
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Query Match 65.7%; Score 1167; DB 6; Length 1455;
Best Local Similarity 87.6%; Pred.No.1.2e-262;
Matches 1275; Conservative 0; Mismatches 180; Indels 0; Gaps 0;

QY 238 CATCATATGGAGAGATGGAGACATGATGATTTTGAATGGCATTTGCCAAATGAC 297
DB 1 CATCATATGGAGAGATGGAGACATGATGATTTTGAATGGCATTTGCCAAATGAC 60
QY 298 GGGAAACACTGGAGACAGTTACGAGATGACGACCTAACTTAAAGATGAAAGGATTTACC 357
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QY 358 GCTGTTGGATTCCTCTGATGAGAGGAGACTTCGCAAAATGATGTTGGTATGTCGCC 417
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QY 1198 CACCTTATACATGACATGACATTTGTTGAATACCATGACTCTCAGCAGAGAAACATTTG 1257
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DB 1141 GCTATGAATCTTAAATTTGATCCACTCTGCAAGGACGTCAAACGATGCTTACGTAAG 1200
QY 1438 CAACATGATTTTATGATCATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1497
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DB 1381 ACCGTCAACATTAAGTGTGCGCAAGTATGAGAGATATTAACGGAATATGATGATGAT 1440
QY 1678 GTTTGGGTGAAGCA 1692
DB 1441 GTTTGGGTGAAGCA 1455

RESULT 15
ARI29912
LOCUS ARI29912 1455 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 9 from patent US 6187576.
ACCESSION ARI29912
VERSION ARI29912.1 GI:14117809
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1455)
AUTHORS Svendsen,A., Borchert,T.Vedel. and Bisg ang.rd-Frantzen,H.
TITLE alpha.-amylase mutants
JOURNAL Patent: US 6187576-A 9 13-FEB-2001;
FEATURES
source location/Qualifiers
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ORIGIN

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: May 2, 2005, 17:25:37 ; Search time 670 Seconds
(without alignments)
15691.732 Million cell updates/sec

Title: US-08-952-741-1

Perfect score: 1776
Sequence: 1 atataaattggaatgacac.....ccaataaattggaagctt 1776

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

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- 1: geneseqn1980s:*
- 2: geneseqn1990s:*
- 3: geneseqn2000s:*
- 4: geneseqn2001as:*
- 5: geneseqn2001bs:*
- 6: geneseqn2002as:*
- 7: geneseqn2002bs:*
- 8: geneseqn2003as:*
- 9: geneseqn2003bs:*
- 10: geneseqn2003cs:*
- 11: geneseqn2003ds:*
- 12: geneseqn2004as:*
- 13: geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	1776	100.0	1776	6 AAD44364 Bacillus
3	1776	100.0	1786	3 AAC66234 Mutant al
4	1776	100.0	1786	6 AAK99881 DNA of Ba
5	1187.2	66.8	6661	10 AAD49392 pMO1995 P
6	1167	65.7	1455	2 AAT00776 Bacillus
7	1167	65.7	1455	2 AAX59636 DNA encod
8	1167	65.7	1455	2 AAX59632 DNA encod
9	1167	65.7	1455	2 AAX57597 wild type
10	1167	65.7	1455	3 AAA48480 Bacillus
11	1167	65.7	1455	3 AAA48485 Bacillus
12	1167	65.7	1455	6 ABL50564 Bacillus
13	1167	65.7	1455	6 AAS20022 Bacillus
14	1167	65.7	1455	6 AAT72211 Bacillus
15	1167	65.7	1455	6 ABL96207 Termany1-
16	1167	65.7	1455	10 ADJ92077 Termany1-
17	1157.4	65.2	1455	2 AAX57592 wild type
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ALIGNMENTS

RESULT 1		AAT51339	
ID	AAT51339	standard; DNA; 1776 BP.	
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AC	AAT51339;		
DT	17-OCT-2003	(revised)	
DT	27-AUG-2003	(revised)	
DT	11-NOV-1997	(first entry)	
XX	XX		
DE	Coding sequence for alkaline liquefying alpha-amylase.		
XX	XX		
KW	Alkaline liquefying alpha-amylase; Bacillus; alpha-amylase; detergent;		
KW	starch-related polysaccharide; hydrolysis; enzyme; surfactant resistance;		
KW	alpha-1,4-glucosidic link; alkalophilic Bacillus; laundry detergent;		
XX	XX		
OS	Bacillus sp; KSM-AP1378.		
XX	XX		
EH	Key	Location/Qualifiers	
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XX	XX		
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PD	03-JAN-1997.		AAA30783 DNA encod
XX	XX		AAC63114 Bacillus
PF	14-JUN-1996;	96MO-JP001641.	ABL50569 Bacillus
XX	XX		AAS20027 Bacillus
PR	14-JUN-1995;	95UP-00147257.	AAT72216 Bacillus
XX	XX		ABL96212 Termany1-
PA	(KAOS) KAO CORP.		ADJ92087 Termany1-
PI	Hatada Y, Ozaki K, Ara K, Kawai S, Ito S;		AAD16805 Bacillus
DR	WPI: 1997-118708/11.		AAD16808 Bacillus
XX	XX		AAX59637 DNA encod
XX	P-PSDB; AAM11326.		AAX59633 DNA encod
PT	DNA encoding alkaline liquefying alpha-amylase - useful in dish-washing		AAX57598 wild type
XX	and laundry detergents for removal of starch dirt.		AAX57593 wild type
XX	Claim 8; Page 23-26; 40pp; English.		AAA48481 Bacillus
PS			AAA48486 Bacillus
			ABL50565 Bacillus
			AAS20023 Bacillus
			AAT72212 Bacillus
			ABL96208 Termany1-
			ADJ92079 Termany1-
			AAC85598 DNA encod
			AAT00777 Bacillus

XX This sequence represents the coding sequence for an alkaline liquefying
CC alpha-amylase. Alpha-amylase is an enzyme that acts on starch-related
CC polysaccharides, hydrolyzing the alpha-1,4-glucoside bond of the
CC polysaccharide molecule. Alkaline liquefying alpha-amylases exhibit
CC resistance to surfactants used in detergents, and decompose starch or
CC starch-related polysaccharides in a highly random manner. The Bacillus
CC species KSM-AP378, from which this sequence was isolated, is an
CC alkalophilic Bacillus strain. It was isolated from soil in the vicinity
CC of the city of Tochi. The enzyme is useful in improving the efficiency
CC of dish-washing and laundry detergents, particularly on starch dirt.
CC (Updated on 27-AUG-2003 to correct OS field.) (Updated on 17-OCT-2003 to
CC standardise OS field)

XX Sequence 1776 BP; 575 A; 305 C; 417 G; 479 T; 0 U; 0 Other;

Query Match 100.0%; Score 1776; DB 2; Length 1776;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1776; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1561 GTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1620
QY 1621 GTTCACATTTATGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1680
DB 1621 GTTCACATTTATGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1680
QY 1681 TGGGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1740
DB 1681 TGGGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1740
QY 1741 CCGATCATCTATACCCATTAATTAATTTGAGAGCTT 1776
DB 1741 CCGATCATCTATACCCATTAATTAATTTGAGAGCTT 1776
RESULT 2
AAD4364 standard; DNA; 1776 BP.
XX
AC AAD4364;
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XX 13-DEC-2002 (first entry)
XX Bacillus species KSM-AP1378 alpha-amylase DNA.
XX Alpha amylase; alpha-1,4-glucan-4-glucanohydrolase; EC 3.2.1.1;
XX dishwashing; textile desizing; detergent; paper; starch liquefaction;
XX laundry; alcohol production; ethanol production; pulp; beer; brewing;
XX Sweetener; enzyme; gene; ds.
OS Bacillus sp.
XX
XX Key Location/Qualifiers
FH 145..1692
FT CDS /*tag= a
FT /product= "KSM-AP1378 alpha-amylase"
FT sig_peptide 145..237
FT /*tag= b
FT mat_peptide 238..1689
FT /*tag= c
FT /product= "Mature KSM-AP1378 alpha-amylase"
FT /EC_number= "3.2.1.1"
XX
XX MO200231124-A2.
XX 18-APR-2002.
XX
XX 12-OCT-2001; 2001MO-DK00668.
XX
XX 13-OCT-2000; 2000DK-00001533.
XX 23-OCT-2000; 2000OU-0242692P.
XX 02-OCT-2001; 2001DK-00001442.
XX 03-OCT-2001; 2001US-0326752P.
XX
XX (NOVO) NOVOZYMES AS.
XX
XX Andersen C;
XX
XX WPI; 2002-463264/49.
XX P-PSDB; AAE26535.
XX
XX KSM-K36 or KSM-K38 variant from Bacillus for cleaning dishes, textile
PT desizing, starch liquefaction and ethanol production has alpha-amylase
PT activity.
XX
XX Disclosure; Page 62-64; 69pp; English.
XX
XX The present invention relates to KSM-K36 or KSM-K38 variant of parent
CC alpha-amylases (alpha-1,4-glucan-4-glucanohydrolases, EC 3.2.1.1) from
CC Bacillus. The variants have alpha-amylase activity and exhibit an amino
CC acid alteration such as an insertion, deletion or substitution of the
CC parent alpha-amylase. The variants are useful for washing and/or dish-
CC washing, textile desizing, starch liquefaction and alcohol production,
CC particularly ethanol production. They are also useful as components in
CC detergents for e.g. laundry, dishwashing and hard surface cleaning
CC divergent compositions, in pulp and paper production, in beer making or
CC brewing and in production of sweeteners. The present sequence is Bacillus
CC species KSM-AP1378 alpha-amylase DNA
XX
XX Sequence 1776 BP; 575 A; 305 C; 417 G; 479 T; 0 U; 0 Other;
SQ
Query Match 100.0%; Score 1776; DB 6; Length 1776;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1776; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 121 AAATGAGAGAGAGGCTTTTATGAACTTCATACCGTATTAATAGCTACTATTA 180
DB |||||
QY 121 AAATGAGAGAGAGGCTTTTATGAACTTCATACCGTATTAATAGCTACTATTA 180
DB |||||
QY 181 ACACTATTTGACCTGAGCTGTTTGTTCATATATGACGAGACGACAAAGCCAT 240
DB |||||
QY 181 ACACTATTTGACCTGAGCTGTTTGTTCATATATGACGAGACGACAAAGCCAT 240
DB |||||
QY 241 CATTAATGGAGCAATGGAGCAATGATGCAATATTTGAATGGATTTGCCAATGACGG 300
DB |||||
QY 241 CATTAATGGAGCAATGGAGCAATGATGCAATATTTGAATGGATTTGCCAATGACGG 300
DB |||||
QY 301 AACCACTGGAACAGTTACAGATGACGACGCTTAATTAAGATTAAGGATTAACGCT 360
DB |||||
QY 301 AACCACTGGAACAGTTACAGATGACGACGCTTAATTAAGATTAAGGATTAACGCT 360
DB |||||
QY 361 GTTTGATTCCTCTGATGGAAGGGGACTTGCAGAAATGATGTTGGATGTCCTAT 420
DB |||||
QY 361 GTTTGATTCCTCTGATGGAAGGGGACTTGCAGAAATGATGTTGGATGTCCTAT 420
DB |||||
QY 421 GATTTGACATCTTGATGATTTAAACCAAAAGGAAACCGTCCGTACAAATATGACCA 480
DB |||||
QY 421 GATTTGACATCTTGATGATTTAAACCAAAAGGAAACCGTCCGTACAAATATGACCA 480
DB |||||
QY 481 AGGAGTCAGTTGCAAGGTCGTCGATCTTTGAAAATTAACGGGATTCAGTTATGG 540
DB |||||
QY 481 AGGAGTCAGTTGCAAGGTCGTCGATCTTTGAAAATTAACGGGATTCAGTTATGG 540
DB |||||
QY 541 GATGTCGATGATCATTAAGGTGAGCAGACGGGACAGAGATGTGTAATGCGGTGAA 600
DB |||||
QY 541 GATGTCGATGATCATTAAGGTGAGCAGACGGGACAGAGATGTGTAATGCGGTGAA 600
DB |||||
QY 601 GTGAACCGAAGCAACGAAACCAAAATATCAGGTGATATACCATTTGAAGCATGGA 660
DB |||||
QY 601 GTGAACCGAAGCAACGAAACCAAAATATCAGGTGATATACCATTTGAAGCATGGA 660
DB |||||
QY 661 AAATTTGATTTCCCTGGAAGAGAAATATCCATTTCCAACTTTAAATGGCCTGTATCAT 720
DB |||||
QY 661 AAATTTGATTTCCCTGGAAGAGAAATATCCATTTCCAACTTTAAATGGCCTGTATCAT 720
DB |||||
QY 721 TTTGATGGAGCAGATTTGGATTCAGTCACGTCAGCTTCAGAACAAATATTAATTGGA 780
DB |||||
QY 721 TTTGATGGAGCAGATTTGGATTCAGTCACGTCAGCTTCAGAACAAATATTAATTGGA 780
DB |||||
QY 781 GGTACCGGAAAGGCAATGGGACTGGGAAATGATATGAGAACCGCAACTATGATTCCT 840
DB |||||
QY 781 GGTACCGGAAAGGCAATGGGACTGGGAAATGATATGAGAACCGCAACTATGATTCCT 840
DB |||||
QY 841 ATGTATGCAACATGTATGATGATCATCCAGATGATATCAATGAACTTAAGATTTGGGGA 900
DB |||||
QY 841 ATGTATGCAACATGTATGATGATCATCCAGATGATATCAATGAACTTAAGATTTGGGGA 900
DB |||||
QY 901 GTTTGATTCACATATCACTTAATCTAGATGATTTAGATTCAGATGCTGTGAACATAT 960
DB |||||
QY 901 GTTTGATTCACATATCACTTAATCTAGATGATTTAGATTCAGATGCTGTGAACATAT 960
DB |||||
QY 961 AAATACGCTATACGAGAGATTTGCTTACACATGTGCTGAACCCACAGGTAAACCAATG 1020
DB |||||
QY 961 AAATACGCTATACGAGAGATTTGCTTACACATGTGCTGAACCCACAGGTAAACCAATG 1020
DB |||||
QY 1021 TTTGCACTTGCAGAAATTTGGAAAAATGACCTTGCTGCAATGCAAAATTAATTAATAA 1080
DB |||||
QY 1021 TTTGCACTTGCAGAAATTTGGAAAAATGACCTTGCTGCAATGCAAAATTAATTAATAA 1080
DB |||||
QY 1081 ACAAGTTGGAATCACTCCGTTGCGATGTTCTCTTCATTAATTAATTTGTAATGCACT 1140
DB |||||
QY 1081 ACAAGTTGGAATCACTCCGTTGCGATGTTCTCTTCATTAATTAATTTGTAATGCACT 1140
DB |||||
QY 1141 AATATGCTGCTATTTGATATGAGAAATATTTAAATGCTTCTGCTGCAAAAACAC 1200
DB |||||
QY 1141 AATATGCTGCTATTTGATATGAGAAATATTTAAATGCTTCTGCTGCAAAAACAC 1200
DB |||||
QY 1201 CTTATACATGCACTCATTTTGTGATTAACCATGACTCTGACGACAGGAAGCATTTGGA 1260

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Db      1201 CCTATACATGACGATCATTTGTTGTAACCATGACTCTCAGCCAGAGAGACATTTGAA 1260
Qy      1261 TCCCTTTGTCATCCGCGTGTCAAACAACGCGCATATGATGATTTCTGACAAAGGAGCA 1320
Db      1261 TCCCTTTGTCATCCGCGTGTCAAACAACGCGCATATGATGATTTCTGACAAAGGAGCA 1320
Qy      1321 GGTATCCCTTCCGATATTTACGCGTGTAACTACGATATACCAATCATGCTGTTCTTGG 1380
Db      1321 GGTATCCCTTCCGATATTTACGCGTGTAACTACGATATACCAATCATGCTGTTCTTGG 1380
Qy      1381 ATGAATCTTAAATTTGATTCATCTTGACGCGCATGCAACGTAATGCTTACGCAACCCAA 1440
Db      1381 ATGAATCTTAAATTTGATTCATCTTGACGCGCATGCAACGTAATGCTTACGCAACCCAA 1440
Qy      1441 CATGATATTTTATGATCATGATATTTATGCGCTGAGCGAGAGAGAGGAGAGCTCCAC 1500
Db      1441 CATGATATTTTATGATCATGATATTTATGCGCTGAGCGAGAGAGAGGAGAGCTCCAC 1500
Qy      1501 CCAATTTGAGACTTGCACATATATATGTCGATGCGCAGAGGAGTAAATGATGAT 1560
Db      1501 CCAATTTGAGACTTGCACATATATATGTCGATGCGCAGAGGAGTAAATGATGAT 1560
Qy      1561 GTGCGGAAACATTAAGCTGCGCAAGTATGAGAGATATCAACGAAATAGCTGTGATCC 1620
Db      1561 GTGCGGAAACATTAAGCTGCGCAAGTATGAGAGATATCAACGAAATAGCTGTGATCC 1620
Qy      1621 GTACACATTAATGACATGCTGGGGGAAATTTCACTGTAACGAGAGGAGATTTGGCTT 1680
Db      1621 GTACACATTAATGACATGCTGGGGGAAATTTCACTGTAACGAGAGGAGATTTGGCTT 1680
Qy      1681 TGGGTAGAGCAATTAATTAAGGACCAAGAGCGAAATTAATTTCTTCTACATGACAGCTT 1740
Db      1681 TGGGTAGAGCAATTAATTAAGGACCAAGAGCGAAATTAATTTCTTCTACATGACAGCTT 1740
Qy      1741 CCGATCACTCAATACCCCAATTAATTTGAGACTT 1776
Db      1741 CCGATCACTCAATACCCCAATTAATTTGAGACTT 1776

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RESULT 3

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AAC66234
ID AAC66234 standard; DNA; 1786 BP.
AC AAC66234;
XX
DT 19-FEB-2001 (first entry)
XX
DE Mutant alpha-amylase nucleotide sequence.
XX
KW Alpha-amylase; detergent; Bacillus; ds.
XX
OS Bacillus sp.
XX
PN JP2000245466-A.
PD 12-SEP-2000.
XX
PF 25-FEB-1999; 99JP-00048213.
XX
PR 25-FEB-1999; 99JP-00048213.
XX
PA (KAOS) KAO CORP.
XX
DR MPI; 2000-615143/59.
XX
DR F-PSDB; AAB35714.
XX
PT A novel mutant alpha-amylase for use in a detergent composition.
XX
PS Example 1; Page 6-9; 12pp; Japanese.
XX
CC The present invention relates to a mutant alpha-amylase. Included in the
CC invention are a gene encoding the mutant alpha-amylase, a vector

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CC containing the gene, and a transformed cell recombinant by the vector. The
 CC enzyme is used in a detergent composition. The present sequence
 CC represents the mutant alpha-amylase gene

SO Sequence 1786 BP; 578 A; 307 C; 420 G; 481 T; 0 U; 0 Other;

Query Match 100.0%; Score 1776; DB 3; Length 1786;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1776; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 ATATTAATTTGAAATGAACCTATGAAATATGATGAGATTTGGCGAGAGAAATAC 60
Db      11 ATATTAATTTGAAATGAACCTATGAAATATGATGAGATTTGGCGAGAGAAATAC 70
Qy      61 TTGGAGATTAGGAAGATATTAAGATTTTGTGACTTGTGTGAAACGCTTGCA 120
Db      71 TTGGAGATTAGGAAGATATTAAGATTTTGTGACTTGTGTGAAACGCTTGCA 130
Qy      121 AAATGGAAGAGAGGCTTTTATGAACTTCATTAACGTAATTAATGCTATTA 180
Db      131 AAATGGAAGAGAGGCTTTTATGAACTTCATTAACGTAATTAATGCTATTA 190
Qy      181 ACACTATTTGTAGCTGTAGCTGTTTGTTCATATATGACGAGACACAGAGCCAT 240
Db      191 ACACTATTTGTAGCTGTAGCTGTTTGTTCATATATGACGAGACACAGAGCCAT 250
Qy      241 CATTAATGGAGACATGAGACATGATGAGATTTTGAATGACATTTGGCAATGACG 300
Db      251 CATTAATGGAGACATGAGACATGATGAGATTTTGAATGACATTTGGCAATGACG 310
Qy      301 AACCACTGGAACAGGTTACGAGATGACGAGCTAACTTAAGATTAAGGATTAACGCT 360
Db      311 AACCACTGGAACAGGTTACGAGATGACGAGCTAACTTAAGATTAAGGATTAACGCT 370
Qy      361 GTTTGATTTCTTCCTGATGAGAGGAGACTTGGCAAAATGATTTGGGATGCTGCT 420
Db      371 GTTTGATTTCTTCCTGATGAGAGGAGACTTGGCAAAATGATTTGGGATGCTGCT 430
Qy      421 GATTTGATGATCTTGGTGTGATTTAACCAAAAGGAGCCGTCCTGACAAATATG 480
Db      431 GATTTGATGATCTTGGTGTGATTTAACCAAAAGGAGCCGTCCTGACAAATATG 490
Qy      481 AGAGAGTCAAGTTCGAGAGTCCGTCGATCTTTGAAATTAACGAGATTCAGTTATG 540
Db      491 AGAGAGTCAAGTTCGAGAGTCCGTCGATCTTTGAAATTAACGAGATTCAGTTATG 550
Qy      541 GATGTCGTATGATATCAATTAAGTGAAGACGAGACGAGATGTTAATGCGTGAA 600
Db      551 GATGTCGTATGATATCAATTAAGTGAAGACGAGACGAGATGTTAATGCGTGAA 610
Qy      601 GTGAACCGAAGACCGAACCAGAAATATGATGATGATACACATTTGAGATGAGAG 660
Db      611 GTGAACCGAAGACCGAACCAGAAATATGATGATGATACACATTTGAGATGAGAG 670
Qy      661 AAATTTGATTTCCCTGGAAGAGAAATACCAATTCACATTTAATGCGCTGTATCAT 720
Db      671 AAATTTGATTTCCCTGGAAGAGAAATACCAATTCACATTTAATGCGCTGTATCAT 730
Qy      721 TTTGATGGAAGATTTGGGATCAAGTCACTGCTGCTGCAACAAATATTAATTA 780
Db      731 TTTGATGGAAGATTTGGGATCAAGTCACTGCTGCTGCAACAAATATTAATTA 790
Qy      781 GGTAACCGAAGAGGATGGAAGTGAAGATATAGAGAACGCAACTATGATTAACCT 840
Db      791 GGTAACCGAAGAGGATGGAAGTGAAGATATAGAGAACGCAACTATGATTAACCT 850
Qy      841 ATGATGACAGATTCATATGATCATCCAGAGATTAATCAATGAATTAATGAGAG 900
Db      851 ATGATGACAGATTCATATGATCATCCAGAGATTAATCAATGAATTAATGAGAG 910
Qy      901 GTTTGATTAACAATTAACATTAATCTAGATGATTTTGAATGATGATGATTAAT 960
Db      911 GTTTGATTAACAATTAACATTAATCTAGATGATTTTGAATGATGATGATTAAT 970

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Qy	961	AAATACAGCTTAAACGAGATTTGGCTAAACATGCGCTAACACACAGTAAACATG	1020
Db	971	AAATACAGCTTAAACGAGATTTGGCTAAACATGCGCTAACACACAGTAAACATG	1030
Qy	1021	TTTGCAGTTGCAGAAATTTTGGAAAAATGACCTTGCTGCAATCGAAAACTATTTAAATPAA	1080
Db	1031	TTTGCAGTTGCAGAAATTTTGGAAAAATGACCTTGCTGCAATCGAAAACTATTTAAATPAA	1090
Qy	1081	ACAAGTGGAAATCACTCCGCTGTGGAGTGTCTCTCACTTAATTTGTAAATGAAGCACT	1140
Db	1091	ACAAGTGGAAATCACTCCGCTGTGGAGTGTCTCTCACTTAATTTGTAAATGAAGCACT	1150
Qy	1141	AATAGTGTGCTATTTTGTATATGAGAAATTTTAAATGCTTGCTGCTGCAAAAAAC	1200
Db	1151	AATAGTGTGCTATTTTGTATATGAGAAATTTTAAATGCTTGCTGCTGCAAAAAAC	1210
Qy	1201	CCATATACATGACATCACTTTGTTGATTAACATGACTCTCAAGCCAGAGAAACATTGGA	1260
Db	1211	CCATATACATGACATCACTTTGTTGATTAACATGACTCTCAAGCCAGAGAAACATTGGA	1270
Qy	1261	TCCATTGTTCAATGCTGTGTAACCACTGGCAATATGCAATGATTCTGACAAAGGAGAA	1320
Db	1271	TCCATTGTTCAATGCTGTGTAACCACTGGCAATATGCAATGATTCTGACAAAGGAGAA	1330
Qy	1321	GGTTAACCCCTTCCGATTTTAAACGATGATTAATCAACGGTATACCACTCATGCTTCCCTCG	1380
Db	1331	GGTTAACCCCTTCCGATTTTAAACGATGATTAATCAACGGTATACCACTCATGCTTCCCTCG	1390
Qy	1381	ATGAATATTAATAATTTGATTCACCTTCTGAGGCAAGTCAACGATATGCTTACGAAACCCA	1440
Db	1391	ATGAATATTAATAATTTGATTCACCTTCTGAGGCAAGTCAACGATATGCTTACGAAACCCA	1450
Qy	1441	CATGATTAATTTGATCATCATGATATTAATGCGCTGAGAGAAAGGGGACAGCTCCAC	1500
Db	1451	CATGATTAATTTGATCATCATGATATTAATGCGCTGAGAGAAAGGGGACAGCTCCAC	1510
Qy	1501	CCAATTCAGAGCTTGCACATTAATATGTCGATGGGCGCAGGGGGTAAATAAATGATGAT	1560
Db	1511	CCAATTCAGAGCTTGCACATTAATATGTCGATGGGCGCAGGGGGTAAATAAATGATGAT	1570
Qy	1561	GTGGGAAACATAAAGCTGCGCAAGTATGAGAGATATCAACCGGAAATAGTCTGTATACC	1620
Db	1571	GTGGGAAACATAAAGCTGCGCAAGTATGAGAGATATCAACCGGAAATAGTCTGTATACC	1630
Qy	1621	GTCAACCATTAATGACGATGTTGGGGGAAATTCACCTGTAAACGAGGGGGCAGTTCCGTT	1680
Db	1631	GTCAACCATTAATGACGATGTTGGGGGAAATTCACCTGTAAACGAGGGGGCAGTTCCGTT	1690
Qy	1681	TGGGTGAAGCAATAAATNAGGAACAGAGGCGGAAATTAATCTTCTCATGACAGCTTT	1740
Db	1691	TGGGTGAAGCAATAAATNAGGAACAGAGGCGGAAATTAATCTTCTCATGACAGCTTT	1750
Qy	1741	CCGATCACTCATCAACCCCAATTAATTTGGAAGCTT	1776
Db	1751	CCGATCACTCATCAACCCCAATTAATTTGGAAGCTT	1786

Accession	Source	Accession	Source
AAK99881	AAK99881 standard; DNA, 1786 BP.	AAK99881	AAK99881
AAK99881	AAK99881	AAK99881	AAK99881
19-JUL-2002	(first entry)	19-JUL-2002	(first entry)
DNA of <i>Bacillus</i> sp alpha-amylase KSM-API378 (FERM BP-3048) protein.		DNA of <i>Bacillus</i> sp alpha-amylase KSM-API378 (FERM BP-3048) protein.	
Alpha-amylase; detergent; laundry; bleaching; dishwashing; enzyme; fibre desizing; starch liquefaction; KSM-API378; FERM BP-3048; gene; ds		Alpha-amylase; detergent; laundry; bleaching; dishwashing; enzyme; fibre desizing; starch liquefaction; KSM-API378; FERM BP-3048; gene; ds	
<i>Bacillus</i> sp.		<i>Bacillus</i> sp.	

Query	Match	100.0%	Score 1776;	DB 6;	Length 1786;
Best Local Similarity	100.0%;	Pred. No. 0;			
Matches 1776;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0	
QY	1 ATATTAATTTGAAATGAAACACCTTATGAAATAATGTTAGCGATTTGGCGACGAGNAAAAAC	60			
DB	11 ATATTAATTTGAAATGAAACACCTTATGAAATAATGTTAGCGATTTGGCGACGAGNAAAAAC	70			
QY	61 TTGGAGTTAGGAAGTATTTAAAGATTTTTTTGACTTTGTTGTGAAAAAGCTTGAT	120			
DB	71 TTGGAGTTAGGAAGTATTTAAAGATTTTTTTGACTTTGTTGTGAAAAAGCTTGAT	130			
QY	121 AAATTTGAGGAGGAGGCTTTTATGAAACTTCATTAACCGTATTAATTAAGGTACTATTA	180			
DB	131 AAATTTGAGGAGGAGGCTTTTATGAAACTTCATTAACCGTATTAATTAAGGTACTATTA	190			
QY	181 ACACATTTAGTTAGCTGTAGCTGTTTGTTCATATATGAGGAAACGACAGACAGCCAT	240			
DB	191 ACACATTTAGTTAGCTGTAGCTGTTTGTTCATATATGAGGAAACGACAGACAGCCAT	250			
QY	241 CATATATGAGGAGGAGGCTTTTATGAAACTTCATTAACCGTATTAATTAAGGTACTATTA	300			
DB	251 CATATATGAGGAGGAGGCTTTTATGAAACTTCATTAACCGTATTAATTAAGGTACTATTA	310			
QY	301 AACCACTGGAACAGGTTACGATATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	360			
DB	311 AACCACTGGAACAGGTTACGATATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	370			

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QY 361 GTTGGATTCTCCGTCATGGAAGGGGACTTGGCAAAATGATGTTGGGTAATGGGCTCAT 420
Db 371 GTTGGATTCTCTCTGATGGAAGGGGACTTGGCAAAATGATGTTGGGTAATGGGCTCAT 430
QY 421 GATTGTAGCATCTTGGTGAATTTAAACCAAAAGGGAACCGTCCGTACAAATAATGACACA 480
Db 431 GATTGTAGCATCTTGGTGAATTTAAACCAAAAGGGAACCGTCCGTACAAATAATGACACA 490
QY 481 AGAAGTCAGTTGGAAGGTGCGGTGACATCTTTGAAAATTAACGGGATTCAGTTTATGGG 540
Db 491 AGAAGTCAGTTGGAAGGTGCGGTGACATCTTTGAAAATTAACGGGATTCAGTTTATGGG 550
QY 541 GATGTGCTGATGATCATTAAGGTGAGACGAGGACAGAGATGGTAAATGCGGTGAA 600
Db 551 GATGTGCTGATGATCATTAAGGTGAGACGAGGACAGAGATGGTAAATGCGGTGAA 610
QY 601 GTGAACCGAAGCAACCGAAACCAAGAAATATCAGTGAATACCAATTGAAAGCATGACG 660
Db 611 GTGAACCGAAGCAACCGAAACCAAGAAATATCAGTGAATACCAATTGAAAGCATGACG 670
QY 661 AATTTGATTTCTCTGGAAGGAATATCCCATTTCCACTTTAAATGGGCTGGTATCAT 720
Db 671 AATTTGATTTCTCTGGAAGGAATATCCCATTTCCACTTTAAATGGGCTGGTATCAT 730
QY 721 TTTGATGGGACAGATTGGGATCAGTCACGTCAGCTTCAGAACCAAAATATTAATTCAGA 780
Db 731 TTTGATGGGACAGATTGGGATCAGTCACGTCAGCTTCAGAACCAAAATATTAATTCAGA 790
QY 781 GGTACCGGAAAGGCATGGGACTGGGAAGTATGATATAGAGAAGCGCAACTATGATTA 840
Db 791 GGTACCGGAAAGGCATGGGACTGGGAAGTATGATATAGAGAAGCGCAACTATGATTA 850
QY 841 AAGTATGAGACATTTGATATGATTCATCCGAAAGTATCAATGAACTTGAATTTGGGGA 900
Db 851 AAGTATGAGACATTTGATATGATTCATCCGAAAGTATCAATGAACTTGAATTTGGGGA 910
QY 901 GTTGTGATACAAATATCACTTAATCAGATGATTTAGAAATCGATCTGGAACAATATT 960
Db 911 GTTGTGATACAAATATCACTTAATCAGATGATTTAGAAATCGATCTGGAACAATATT 970
QY 961 AATATACAGCTATATCGAAGATTGGCTTAACATATGCTGTAACCAACAGGTAAACCAATG 1020
Db 971 AATATACAGCTATATCGAAGATTGGCTTAACATATGCTGTAACCAACAGGTAAACCAATG 1030
QY 1021 TTTGCAAGTGCAGAAATTTTGGAAATATGACCTTGGCAATGGAATTAATTAATAA 1080
Db 1031 TTTGCAAGTGCAGAAATTTTGGAAATATGACCTTGGCAATGGAATTAATTAATAA 1090
QY 1081 ACAAGTTGGAAATCACTCCGTTGTCAGATGTTCTCTCATTAATTAATTTGTAACATGATCT 1140
Db 1091 ACAAGTTGGAAATCACTCCGTTGTCAGATGTTCTCTCATTAATTAATTTGTAACATGATCT 1150
QY 1141 AATAGTGTGGCTATTTTGTATGAGAATATTTTAAATGATCTGTCTGTAACAAAACAC 1200
Db 1151 AATAGTGTGGCTATTTTGTATGAGAATATTTTAAATGATCTGTCTGTAACAAAACAC 1210
QY 1201 CCTATACATGACATCATTTGTTGTAATCAATGACCTTCAGCAGAGAGAAGCATTTGAA 1260
Db 1211 CCTATACATGACATCATTTGTTGTAATCAATGACCTTCAGCAGAGAGAAGCATTTGAA 1270
QY 1261 TCCTTTGTCAATCGTGTCAAAACCACTGGCATATGCAATTTGTAACAAGGAGCAA 1320
Db 1271 TCCTTTGTCAATCGTGTCAAAACCACTGGCATATGCAATTTGTAACAAGGAGCAA 1330
QY 1321 GGTACCCCTTCGTAATTTTACGGTATTAATCAAGTATACCAATCAATGATGTTCTTGG 1380
Db 1331 GGTACCCCTTCGTAATTTTACGGTATTAATCAAGTATACCAATCAATGATGTTCTTGG 1390
QY 1381 ATGAATCTTAAATTTGATCACTTTCGACGAGCAATGCAACGATACGTAACGAAACCAA 1440
Db 1391 ATGAATCTTAAATTTGATCACTTTCGACGAGCAATGCAACGATACGTAACGAAACCAA 1450

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QY 1441 CATGATTATTTTATCATCATGATATTAATCGGCTGGAAGGAGGAGGACAGCTCCAC 1500
Db 1451 CATGATTATTTTATCATCATGATATTAATCGGCTGGAAGGAGGAGGAGGACAGCTCCAC 1510
QY 1501 CCAATTCAGACTTGCACATTAATATGTCGATGGGCCAGGGGGTAAATATGATGAT 1560
Db 1511 CCAATTCAGACTTGCACATTAATATGTCGATGGGCCAGGGGGTAAATATGATGAT 1570
QY 1561 GTGGGGAACATTAAGCTGGCCAGATGAGAGATATCACGGGAATATGATGATGAT 1620
Db 1571 GTGGGGAACATTAAGCTGGCCAGATGAGAGATATCACGGGAATATGATGATGAT 1630
QY 1621 GTACACATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1680
Db 1631 GTACACATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1690
QY 1681 TGGGTGAGCAATTAATTAAGGAACAAGAGGCAAAATTAATTTCTTCTCATGACAGCTTT 1740
Db 1691 TGGGTGAGCAATTAATTAAGGAACAAGAGGCAAAATTAATTTCTTCTCATGACAGCTTT 1750
QY 1741 CCGATCCTCATACACCCCAATTAATTTGGAAGCTT 1776
Db 1751 CCGATCCTCATACACCCCAATTAATTTGGAAGCTT 1786

RESULT 5
AAD49392/c
ID AAD49392 standard; DNA; 6661 bp.
XX AC
XX AAD49392;
XX AC
XX 07-MAR-2003 (first entry)
XX DE
XX PMOL995 plasmid DNA.
XX KW
XX Pectate lyase; EC 4.2.2.2; detergent; surfactant; cleaning; dishwashing;
KW fabric stain removal; fabric whiteness maintenance; fabric softening;
KW fabric colour appearance; fabric dye transfer inhibition; de-pilling;
KW dental application; oral application; colour clarification; enzyme;
KW clay stain removal; ds.
XX OS
XX Unidentified.
XX FH
XX Key Location/Qualifiers
FT 1..1962
FT misc_feature /tag= a
FT /note= "Encodes PUB110 plasmid"
FT 1963..2305
FT terminator /tag= b
FT /note= "Encodes transcriptional terminator from amyL gene
FT of B. licheniformis ATCC14580 and a few introduced
FT restriction sites"
FT 2306..3766
FT misc_feature /tag= c
FT /note= "Encodes mature part of alpha-amyase"
FT complement (3767..4075)
FT /tag= d
FT /note= "Encodes the promoter and signalpeptide of alpha-
FT amyase"
FT 4076..6661
FT /tag= e
FT /note= "Encodes PUB110 plasmid"
XX PN
XX MO20029741-A2.
XX PD
XX 21-NOV-2002.
XX PF
XX 14-MAY-2002; 2002WO-DK000315.
XX PR
XX 14-MAY-2001; 2001DK-00000755.
XX PR
XX 14-MAY-2001; 2001US-0290738P.
XX PA
XX (NOVO ) NOVOZYMES AS.

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XX Eskelund MB, Schuelein M, Nielsen VS, Smets J;
XX WPI: 2003-059005/05.
XX
XX New polypeptide useful as ingredient of detergent composition for
XX cleaning fabric, dishware or hard surface, encoded by DNA sequence
XX endogenous to strain of *Bacillus subtilis*, comprises pectate lyase
XX activity.
XX
XX Disclosure: Page 84-87; 95pp; English.
XX
XX The present invention relates to pectate lyase (EC 4.2.2.2) proteins and
XX polynucleotides encoding such proteins. The invention also relates to
XX detergent compositions comprising a surfactant and pectate lyase enzyme.
XX The detergent is useful for cleaning a fabric, a dishware or hard surface
XX to provide superior cleaning performance, for fabric cleaning and/or
XX fabric stain removal and/or fabric whiteness maintenance and/or fabric
XX softening and/or fabric color appearance and/or fabric dye transfer
XX inhibition, for cleaning hard surfaces such as floors, walls or bathroom
XX tiles, for hand and machine dishwashing and for oral and/or dental
XX applications. They are useful for colour clarification, de-pilling and in
XX clay stain removal. The present sequence is pMOJ995 plasmid DNA
XX
XX Sequence 6661 BP; 1859 A; 1534 C; 991 G; 2277 T; 0 U; 0 Other;
XX
Query Match 66.8%; Score 1187.2; DB 10; Length 6661;
Basic Local Similarity 84.1%; Pred. No. 1.4e-312;
Matches 1339; Conservative 0; Mismatches 253; Indels 0; Gaps 0;
QY 119 ATAATTGAGAGAGGGGCTTTTATGAACTTCAATACCGTATATAGCTACTAT 178
DB 3882 AGAAATGAGAGGAGAGGAAATGATTCATCAAAACGAGACGTTCTTCAGAC 3823
QY 179 TAACATATTGTTAGCTGAGCTGTTTGTTCATATATGACGGAACGACACAGCCC 238
DB 3822 TTGCTATATGACGCTGTTATTTGTCACTTGGCATTAACAAAACATCCCGGCC 3763
QY 239 ATCATATGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 298
DB 3762 ATCATATGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3703
QY 299 GGAACCACTGAGAGAGGTTAGAGATGACGAGCTTAATTAAGTAAAGGATTAACG 358
DB 3702 GGAATCATGAGAGAGGTTAGAGATGACGAGCTTAATTAAGTAAAGGATTAACG 3643
QY 359 CTGTTGAGATTCCTCTGATGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 418
DB 3642 CTGATGAGATCCACCTGATGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3583
QY 419 ATGATTTGATGAGATCTGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 478
DB 3582 ATGATTTGATGAGATCTGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3523
QY 479 CAAGAGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 538
DB 3522 CAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3463
QY 539 GGGATGTCGATGAGATCATTAAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 598
DB 3462 GTGATGTCGATGAGATCATTAAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3403
QY 599 AAGTGAACCGAG 658
DB 3402 AAGTGAACCGAG 3343
QY 659 CGAATATGATTTCCCTGAG 718
DB 3342 CAAAGTTGATTTCTCTGAG 3283
QY 719 ATTTGATGAG 778
DB 3282 ATTTGATGAG 3223

QY 779 GAGGTACCGAG 838
DB 3222 GGGAG 3163
QY 839 TTATGATGAG 898
DB 3162 TTATGATGAG 3103
QY 899 GAGTTGGTATCAATATCACTTATATCTAGATGATTTAGATGATGCTGTGAACATA 958
DB 3102 GAGTGTGATCAATATCACTTATATCTAGATGATTTAGATGATGCTGTGAACATA 3043
QY 959 TTAATACAGTATACAG 1018
DB 3042 TAAATATAGCTTTACAG 2983
QY 1019 TGTTCAGATGAG 1078
DB 2982 TGTTCAGATGAG 2923
QY 1079 AAGCAAGTGGATCACTCCGTTGATGATGTTCTCTTCAATATATTTGTAATGATCAT 1138
DB 2922 AAGCAAGTGGATCACTCCGTTGATGATGTTCTCTTCAATATATTTGTAATGATCAT 2863
QY 1139 CTATAGTGGTGGCTATTTTATGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1198
DB 2862 CTATAGTGGTGGCTATTTTATGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2803
QY 1199 ACCCTATACAG 1258
DB 2802 ATCAACAG 2743
QY 1259 AATCTTTGTTCAATCGTGTGTAACCACTGAGATGATGATGATGATGATGATGATGAT 1318
DB 2742 AATCTTTGTTCAATCGTGTGTAACCACTGAGATGATGATGATGATGATGATGATGAT 2683
QY 1319 AAGGTACCTCTGATTTTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1378
DB 2682 AAGGTACCTCTGATTTTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2623
QY 1379 CGATGAATCTAAATATGATCACTTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1438
DB 2622 CTATGAATCTAAATATGATCACTTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2563
QY 1439 AACTGATATTTTATGATCACTTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1498
DB 2562 AACTGATATTTTATGATCACTTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2503
QY 1499 ACCCAATTCAG 1558
DB 2502 ATCCAAATTCAG 2443
QY 1559 ATGTCGAG 1618
DB 2442 ATGTCGAG 2383
QY 1619 CCGTCACATTAATGAG 1678
DB 2382 CCGTCACATTAATGAG 2323
QY 1679 TTTGGTGAAGCAATTAATGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1710
DB 2322 TTTGGTGAAGCAATTAATGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2291

RESULT 6
AAT00776
ID AAT00776 standard; DNA, 1455 BP.
XX
XX AAT00776;
XX
DT 16-MAR-1996 (first entry)

XX DE Bacillus sp. alkaline alpha-amylase DNA.
 XX KW Alpha-amylase; enzyme; EC-3.2.1.1; detergent; surfactant; textile; beer;
 XX KM starch; ss.
 XX OS Bacillus.
 XX PN MO9526397-AI.
 XX PF 29-MAR-1995; 95MO-DK000142.
 XX PR 29-MAR-1994; 94DK-00000353.
 XX PR 03-NOV-1994; 94DK-00001271.
 XX PR 03-FEB-1995; 95DK-00000123.
 XX PA (NOVO) NOVO-NORDISK AS.
 XX PI Outtrup H, Bisgard-Frantzen H, Ostergaard PR, Rasmussen MD;
 XX PI Van Der Zee P;
 XX DR MPI; 1995-351318/45.
 XX DR P-PSDB; AAR81835.
 XX PT New alkaline Bacillus alpha-amylase - used in e.g. detergent compns.
 XX PT starch liquefaction, textile desizing, starch modification or beer
 XX PT making.
 XX PS Disclosure; Page 48-49; 65pp; English.
 XX PS This DNA sequence may be expressed recombinantly for the production of an
 CC alpha-amylase protein. The produced protein is characterized by having a
 CC specific activity at least 25% higher than the specific activity of
 CC Termamyl at 25-55 deg C and a pH of 8-10. The enzyme can be used in
 CC detergent composition for starch liquefaction, the production of
 CC lignocellulosic materials, e.g. pulp, paper and cardboard from waste
 CC containing starch, for deinking recycled starch-coated, or starch-
 CC containing printed paper, to modify starch for papermaking, for textile
 CC desizing, and beer-making processes
 CC XX
 SQ Sequence 1455 BP; 461 A; 248 C; 361 G; 385 T; 0 U; 0 Other;
 Query Match 65.7%; Score 1167; DB 2; Length 1455;
 Best Local Similarity 87.6%; Pred. No. 2.5e-307;
 Matches 1275; Conservative 0; Mismatches 180; Indels 0; Gaps 0;

DB 361 GAAGTGAATCGGAGCAACCGAAACGAGAACCTGAGAGATATGCAATAGAGCGTGG 420
 QY 658 ACGAAATTTGATTTCCCTGGAGAGAGAAATACCATTTCACTTTAAATGGCGTGTAT 717
 DB 421 ACAAGTTTGAATTTCTTGGAAGAGAAATACATCTCCAGCTTTAAAGGCGGTGTAT 480
 QY 718 CATTTTGAATGAGACGATTTGGGATCAGTCACTGACCTTCAGAACCAATATATTAATTC 777
 DB 481 CATTTTGAATGAGACGATTTGGGATCAGTCACTGACCTTCAGAACCAATATATTAATTC 540
 QY 778 AGAGTACCGGAAAGGATGGGACTGGGAGATGATATAGAGAACGGCACTATGATTAC 837
 DB 541 AGGGGAAACAGGAGGCGCTGGGACTGGGAGATGATATAGAGAAATGGCAACTATGACTAT 600
 QY 838 CTTATGTATGACAGACATTTATATGATCATCCAGAAATATCAATGAATCTTGAATTTGG 897
 DB 601 CTTATGTATGACAGCGTGTATGATCACTCCAGAAATATCAATGAATCTTGAATTTGG 660
 QY 898 GGAGTTTGTATCAAAATACCTTAATCTAGATGATTTAGAAATGATGATGCTGTGAACAT 957
 DB 661 GGAGTGTGTATGACGATACCTGAACTGTAACCTTATGATTTAGATATGATGCAATGTAACAT 720
 QY 958 ATTAATACAGCTATACAGAGATTTGCTTACACATGTGCTTACACACAGATAAACCA 1017
 DB 721 ATTAATATAGCTTTACAGAGATTTGCTTACACATGTGCTTACACACAGATAAACCA 780
 QY 1018 ATGTTTGCAGTTGCAGAAATTTTGGAAAAATGACCTTGTGCAATGGAATCTTTAAAT 1077
 DB 781 ATGTTTGCAGTTGCAGAAATTTTGGAAAAATGACCTTGTGCAATGGAATCTTTAAAT 840
 QY 1078 AAAACAAGTTGGAATCACTCCGTTGCTGATGTTCCCTTCATTAATATTTTGAATGCA 1137
 DB 841 AAAACAAGTTGGAATCACTCCGTTGCTGATGTTCCCTTCATTAATATTTTGAATGCA 900
 QY 1138 TCTAATAGTGTGGCTATTTTGAATGAGAAATTTTAAATGTTTGTGCTTACAAAAA 1197
 DB 901 TCTAATAGTGTGGCTATTTTGAATGAGAAATTTTAAATGTTTGTGCTTACAAAAA 960
 QY 1198 CACCTTATACAGACGTCATTTTGTGATTAACATGACTCTCAGCCAGAGAAATGATG 1257
 DB 961 CATCAACACATGCGGTATCTTTGTGTATTAACATGATTCACGCCGCGGAGACATTTG 1020
 QY 1258 GAATCCTTTGTCATACGTCGTTCAAAACCATGCGATATGATGATTTCTGACAAAGGAG 1317
 DB 1021 GAATCCTTTGTCATACGTCGTTCAAAACCATGCGATATGATGATTTCTGACAAAGGAG 1080
 QY 1318 CAAGTTTACCTTCCGTATTTTACGCTGATTAATAAGGTATACCACTGATGCTTCT 1377
 DB 1081 CAAGTTTACCTTCCGTATTTTACGCTGATTAATAAGGTATACCACTGATGCTTCT 1140
 QY 1378 TCGATGAATCTTAAATGATCACTTCTGACAGGACCGTCAACGATATGCTTACGGAAC 1437
 DB 1141 GGTATGAATCTTAAATGATCACTTCTGACAGGACCGTCAACGATATGCTTACGGAAC 1200
 QY 1438 CAACATGATTTTATGATCATGATATTTATCGCTGAGCAGAGAAAGGAGGACGCTCC 1497
 DB 1201 CAGCATGATTTATTTGATCATGATATTTATCGCTGAGCAGAGAAATGAGCTCC 1260
 QY 1498 CACCAATTCAGACTTGCAACTTATGTCGATGAGGCGCAGGCGGTATTAATGATG 1557
 DB 1261 CATCAAAATTCAGGCTTGCCACCACTTATGTCGATGAGGCGCAGGCGGTATTAATGATG 1320
 QY 1558 TATGTGCGGGAACATTAAGCTGCGCAAGATAGAGATATCAACGGAATATGCTGTGCT 1617
 DB 1321 TATGTGCGGGAACATTAAGCTGCGCAAGATAGAGATATTAACGGAATATGAGCTG 1380
 QY 1618 ACCGTCAACATTAATGAGATGTTGGGGAATTTCACTGTAAACGAGGCGCAAGTTTCG 1677
 DB 1381 ACCGTCAACATTAATGAGATGTTGGGGAATTTCTGTATTAATGAGGCGCAAGTTTCG 1440
 QY 1678 GTTGGGTGAACAA 1692

Db 1441 GTTGGGTGAAGCAA 1455

RESULT 7
ID AAX59636 standard; DNA; 1455 BP.
XX AAX59636;
AC AAX59636;
XX 22-JUL-1999 (first entry)
DT
XX DNA encoding a termamyl-like alpha-amylase protein.
DE
XX Termamyl-like; alpha-amylase; variant; washing; dishwashing; production;
KM sweetener; ethanol; starch; textile desizing; starch liquefaction;
KM saccharification process; ss.
XX Bacillus sp.
OS
XX MO9923211-AL.
PN
XX 14-MAY-1999.
PD
XX 30-OCT-1998; 98WO-DK000471.
PF
XX 30-OCT-1997; 97DK-00001240.
PR 14-JUL-1998; 98DK-00000936.
XX
XX (NOVO) NOVO-NORDISK AS.
PA
XX Borchert TV, Svendsen A, Andersen C, Nielsen BR, Nissen TL;
PI Kjaerulff S;
XX WPI; 1999-326987/27.
DR
XX New Termamyl-like alpha-amylase variants.
PS
XX Disclosure; Page 98; 115pp; English.
XX The specification describes termamyl-like alpha-amylase variants that
CC have altered amino acid sequences to improve properties. The variants are
CC produced by creating one or more of the following mutations in amino acid
CC sequence of the parent termamyl-like alpha-amylase: T141, K142, F143,
CC D144, P145, P146, G147, R148, G149, Q174, R181, G182, D183, G184, K185,
CC A186, W188, S193, N195, H107, K108, G109, D166, W167, D168, Q169, S170,
CC R171, Q172, F173, F267, W268, K269, N270, D271, L272, G273, A274, L275,
CC K311, E346, K385, G456, W457, K458, P459, G460, T461, V462, T463. The
CC variants can be used for washing and/or dishwashing. They can also be
CC used in the production of sweeteners and ethanol from starch, and/or for
CC textile desizing, and in starch liquefaction and/or saccharification
CC processes. The present sequence encodes an amylase that can function as
CC the parent sequence in the production of the variants of the invention
XX
SQ Sequence 1455 BP; 461 A; 248 C; 361 G; 385 T; 0 U; 0 Other;

Query Match 65.7%; Score 1167; DB 2; Length 1455;
Best Local Similarity 87.6%; Pred. No. 2.5e-307;
Matches 1275; Conservative 0; Mismatches 180; Indels 0; Gaps 0;

QY 238 CATCATATATGAGAGATGGAGCCATGATGAGATTTTGAATGGCATTTGCCAAATGAC 297
Db 1 CATCATATATGAGAGAGATGGAGCCATGATGAGATTTTGAATGGCATTTGCCAAATGAC 60

QY 298 GGAAGCACTGGAACAGGTTACGAGATGACGAGCTTAATTAAAGATTAAGGATTAAC 357
Db 61 GGAAGCACTGGAACAGGTTACGAGATGACGAGCTTAATTAAAGATTAAGGATTAAC 120

QY 358 GCTGTTTGATTCCTCTCGATGAGAGGAGCTTGCAAAATGATTTGGGTATGATGCC 417
Db 121 GCTGTTTGATTCCTCTCGATGAGAGGAGCTTGCAAAATGATTTGGGTATGATGCC 180

QY 418 TATGATTTGATGATCTTGTGATGATTTTAACCAAAAGGAAACGTCCTGACAAATATGAC 477
Db 418 TATGATTTGATGATCTTGTGATGATTTTAACCAAAAGGAAACGTCCTGACAAATATGAC 477

Db 181 TATGATTTATATGATCTTGGAGAGCTTTAACCAAGAGGAGCGTTCGTACAAATATGCA 240

QY 478 ACAGAGATGATGATGCAAGGCGCGTGACATCTTTGAAAAATACGGGATTCAGTTTAT 537
Db 241 ACAGAGATGATGATGCAAGGCGCGTGACATCTTTGAAAAATACGGGATTCAGTTTAT 300

QY 538 GGGATGTCGTATGATTAATTAAGGTGAGACAGGAGCAGAGATGTTAAATGCGGTG 597
Db 301 GGTATGTCGTATGATTAATTAAGGTGAGACAGGATGTTAAATGCGGTG 360

QY 598 GAAGTGAACCGAAGCAACCGAAGCAAAATATCAGGTGATACCATTTAAGCATGG 657
Db 361 GAAGTGAACCGAAGCAACCGAAGCAAAATCAGGTGATACCATTTAAGCATGG 420

QY 658 ACGAAATTTGATTTCCCTGGAAGGAAATTAACCATTCGAACTTTAATGCGGTGAT 717
Db 421 ACGAAATTTGATTTCCCTGGAAGGAAATTAACCATTCGAACTTTAATGCGGTGAT 480

QY 718 CATTTGATGAGACAGATGGGATCAGTCACTGAGCTTCAGAACAAATATATTAATTC 777
Db 481 CATTTGATGAGACAGATGGGATCAGTCACTGAGCTTCAGAACAAATATATTAATTC 540

QY 778 AGAGATACCGGAAAGGATGGGAGCTGGGAAGTATAGAAACGCACTATGATTAC 837
Db 541 AGGGAACAGGCAAGGCTGGGAGCTGGGAAGTATAGAAACGCACTATGATTAC 600

QY 838 CTTATGATGAGACATTTGATTAATGATTAATGATTAATGATTAATGATTAATG 897
Db 601 CTTATGATGAGACATTTGATTAATGATTAATGATTAATGATTAATGATTAATG 660

QY 898 GGAATTTGATTAATGATTAATGATTAATGATTAATGATTAATGATTAATGATTAAT 957
Db 661 GGAATTTGATTAATGATTAATGATTAATGATTAATGATTAATGATTAATGATTAAT 720

QY 958 ATTAATATACAGCTTATACAGATGATGATGATGATGATGATGATGATGATGAT 1017
Db 721 ATTAATATACAGCTTATACAGATGATGATGATGATGATGATGATGATGATGAT 780

QY 1018 ATGTTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1077
Db 781 ATGTTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 840

QY 1078 AAAACAAGTGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1137
Db 841 AAAACAAGTGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 900

QY 1138 TCTAATAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 1197
Db 901 TCTAATAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 960

QY 1198 CACCTTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1257
Db 961 CACCTTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1020

QY 1258 GAATCCTTTGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1317
Db 1021 GAATCCTTTGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1080

QY 1318 CAAGTTTACCTTCCGATTTTAAAGTATGATGATGATGATGATGATGATGATGATGAT 1377
Db 1081 CAAGTTTACCTTCCGATTTTAAAGTATGATGATGATGATGATGATGATGATGATGAT 1140

QY 1378 TCGATGAATCTAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1437
Db 1141 TCGATGAATCTAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1200

QY 1438 CAAGATGATTTTAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1497
Db 1201 CAAGATGATTTTAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1260

QY 1498 CACCAAAATTCAGACTTGAACATTAATGATGATGATGATGATGATGATGATGATGATGAT 1557
Db 1261 CACCAAAATTCAGACTTGAACATTAATGATGATGATGATGATGATGATGATGATGATGAT 1320


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DB 1021 GAATCCTTTGTCACAGATGGTTTAAACCACTTGATGATGGTTGTCGACAGGSA 1080
QY 1318 CAAGTTTACCTTCGATTTTACGGTATCTACGGTATACCACTCATGTTCTT 1377
DB 1081 CAAGTTTACCTTCGATTTTACGGTATCTACGGTATACCACTCATGTTCTT 1140
QY 1378 TCGATGAATCTTAAATTTGATTCACCTTCGACAGGACGTAAAGTATGCTACGAA 1437
DB 1141 GCTATGAATCTTAAATTTGATTCACCTTCGACAGGACGTAAAGTATGCTACG 1200
QY 1438 CAACATGATTTTATGATCATCATGATTTATGCTGAGAGAGAGAGAGAGAGAG 1497
DB 1201 CAGCATGATTTATCTTATGATCATGATTTATGCTGAGAGAGAGAGAGAGAGAG 1260
QY 1498 CACCAATTCAGAGCTTGTACATTTATGCTGAGAGAGAGAGAGAGAGAGAG 1557
DB 1261 CATCAATTCAGAGCTTGTACATTTATGCTGAGAGAGAGAGAGAGAGAGAG 1320
QY 1558 TATGTGGGAGAAATTAAGCTGGCAAGTATGAGAGATTCACCGGAAATAGCTGG 1617
DB 1321 TATGTGGGAGAAATTAAGCTGGCAAGTATGAGAGATTCACCGGAAATAGCA 1380
QY 1618 ACCGTACCATTTATGATGATGTTGGGGAATTTCACTGTAAACGAGGGGAGTT 1677
DB 1381 ACCGTACCATTTATGATGATGTTGGGGAATTTCTCTGTTAATGAGGGGTCG 1440
QY 1678 GTTTGGGTGAGCAA 1692
DB 1441 GTTTGGGTGAGCAA 1455

RESULT 10
AAA48480
ID AAA48480 standard; DNA; 1455 BP.
XX AAA48480;
AC 04-SEP-2000 (first entry)
DT 04-SEP-2000 (first entry)
XX 04-SEP-2000 (first entry)
DE Bacillus parent Teramyl-like alpha-amylase DNA sequence #1.
XX Bacillus; alpha-amylase; washing; textile desizing; starch liquefaction;
KM saccharification; muten; mutant; enzyme stability; hybrid; ss.
XX Bacillus sp.
OS Bacillus sp.
FH Key Location/Qualifiers
FT CDS 1..1455
FT 1..1455
FT /product= "Teramyl-like alpha-amylase"
FT /partial
XX WO200029560-A1.
XX 25-MAY-2000.
XX 16-NOV-1999; 99WO-DK000628.
XX 16-NOV-1998; 98DK-00001495.
XX (NOVO ) NOVO-NORDISK AS.
XX Svendsen A, Kjaerulf S, Bisgard-Frantzen H, Andersen C;
XX WPI; 2000-387777/33.
XX P-PSDB; AAY99602.
XX Variant of parent teramyl-like alpha amylase useful for washing, textile
XX desizing and starch liquefaction, comprising alterations in one or more
XX solvent exposed amino acid residues.
XX Disclosure; Page 65-66; 80pp; English.
XX
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CC The present sequence encodes a parent Teramyl-like alpha-amylase from
CC which mutants with increased stability at acidic pH, low calcium
CC concentration and high temperatures have been derived. The sequence was
CC isolated from a Bacillus genomic DNA library. A variant may contain
CC mutations in one or more solvent exposed amino acid residues to increase
CC the overall hydrophobicity of the enzyme or the overall number of methyl
CC groups in the side chains of exposed residues may be increased. The
CC mutations can be incorporated by site-directed mutagenesis or by random
CC mutagenesis. As a result of their increased stability, the variants are
CC suitable for the industrial processing of starch, i.e. starch
CC liquefaction and saccharification. They may also be useful for washing,
CC dishwashing and textile desizing. Hybrid alpha-amylases comprising
CC partial amino acid sequences derived from two or more alpha-amylases have
CC also been created in order to increase enzyme stability
XX
SQ Sequence 1455 BP; 461 A; 248 C; 361 G; 385 T; 0 U; 0 Other;
Query Match 65.7%; Score 1167; DB 3; Length 1455;
Best Local Similarity 87.6%; Pred. No. 2.5e-307;
Matches 1275; Conservative 0; Mismatches 180; Indels 0; Gaps 0;
QY 238 CATCATTAATGGAACGATGGAACCATGATGCGATTTTGAATGGCATTTGCCAATGAC 297
DB 1 CATCATTAATGGAACGATGGAACCATGATGCGATTTTGAATGGCATTTGCCAATGAC 60
QY 298 GGGAACCACTGGAACGTTAGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 357
DB 61 GGGAAATCATGGAACGTTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 120
QY 358 GGTGTTGGATTCCTCTCATATGGAAGGGAGCTTGCAGAAATGATGTTGGTATGCTG 417
DB 121 GGTGTTGGATTCCTCTCATATGGAAGGGAGCTTGCAGAAATGATGTTGGTATGCTG 180
QY 418 TATGATTTGATGATTTTGTGATTTTAAACCAAAAGGAGACCGTCCGTCAAAATATG 477
DB 181 TATGATTTGATGATTTTGTGATTTTAAACCAAAAGGAGAGAGAGAGAGAGAGAG 240
QY 478 ACAAGAGTCAATGTCAGAGTCCGTCATCTTTGAAATTAACGGAGTTCAAGTTAT 537
DB 241 ACAAGAGTCAATGTCAGAGTCCGTCATCTTTGAAATTAACGGAGTTCAAGTTAT 300
QY 538 GGGAGTGTGATGATGATTAAGTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 597
DB 301 GGTGATGTCGTATGATCATTAAGAGTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 360
QY 598 GAAGTAAACCGAAGCAACCGAAGCAATATGAGTGAATACCCATTGAAGATGAG 657
DB 361 GAAGTAAACCGAAGCAACCGAAGCAATATGAGTGAATACCCATTGAAGATGAG 420
QY 658 ACAAAATTTGATTTTCTCTGGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 717
DB 421 ACAAAATTTGATTTTCTCTGGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 480
QY 718 CATTTTATGAGGAGATGAGATGAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGT 777
DB 481 CATTTTATGAGGAGATGAGATGAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGT 540
QY 778 AAGAGTAAACCGAAGCAACCGAAGCAATATGAGTGAATACCCATTGAAGATGAG 837
DB 541 AAGAGTAAACCGAAGCAACCGAAGCAATATGAGTGAATACCCATTGAAGATGAG 600
QY 838 CTTATGATGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 897
DB 601 CTTATGATGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 660
QY 898 GGAATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 957
DB 661 GGAATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 720
QY 958 ATTAATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGAT 1017
DB 721 ATTAATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGAT 780
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QY 778 AGAGTACCGGAAGGCGATGGGAGTGAATGATATAGAGAACGGCAATTAATGATTAC 837
DB 541 AGGGGAAACAGGAGGCGCTGGGAGCTGGAGAGTGCATACAGAGATGGCAACTATATGCTAT 600
QY 838 CTATATGATGAGACAGATTAATGATATGATATCCAGAGATTAATCAATCACTTAAGAAATGG 897
DB 601 CTATATGATGAGACAGATTAATGATATGATATCCAGAGATTAATCAATCACTTAAGAAATGG 660
QY 898 GGAGTTGGTATACAAATACCTTAATCTAGATGATGATTAAGATTCAGTCTGTGAACAT 957
DB 661 GGAGTTGGTATACAAATACCTTAATCTAGATGATGATTAAGATTCAGTCTGTGAACAT 720
QY 958 ATTAAATACAGCTATGAGAGATTTGGCTTAACAGATGGGTACACCAAGGTAACCA 1017
DB 721 ATTAAATACAGCTATGAGAGATTTGGCTTAACAGATGGGTACACCAAGGTAACCA 780
QY 1018 ATGTTGACAGTTCAGAAATTTTGGAAAAATGACCTTGCTGCAATCGAAAACTATTTAAT 1077
DB 781 ATGTTGACAGTTCAGAAATTTTGGAAAAATGACCTTGCTGCAATCGAAAACTATTTAAT 840
QY 1078 AAAACAGTTGGATCACTCCGTTCGATGTTCTCTTCATTAATTAATTTGTAATGCA 1137
DB 841 AAAACAGTTGGATCACTCCGTTCGATGTTCTCTTCATTAATTAATTTGTAATGCA 900
QY 1138 TCTAATAGTGGGCTTAATTTGATAGAGAAATTTTAAATGCTCTGTCGTAAGAAA 1197
DB 901 TCTAATAGTGGGCTTAATTTGATAGAGAAATTTTAAATGCTCTGTCGTAAGAAA 960
QY 1198 CACCCTATACATGACATCAATTTGTTGATTAACATGATGATCTGACGACAGAGAGATTTG 1257
DB 961 CACCCTATACATGACATCAATTTGTTGATTAACATGATGATCTGACGACAGAGAGATTTG 1020
QY 1258 GAATCTTTGTTGATGATGTTCAAACTGGCATATGATGATTTCTGACAGAGAG 1317
DB 1021 GAATCTTTGTTGATGATGTTCAAACTGGCATATGATGATTTCTGACAGAGAG 1080
QY 1318 CAAGGTTACCTTCGCTATTTTACGGTATTAAGATTAACATGATGATTTCTGACAGAGAG 1377
DB 1081 CAAGGTTACCTTCGCTATTTTACGGTATTAAGATTAACATGATGATTTCTGACAGAGAG 1140
QY 1378 TCGATGAATATTAATTAATGATTCATCTGTCAGAGAGATTAACATGATGATTTCTGACAGAGAG 1437
DB 1141 TCGATGAATATTAATTAATGATTCATCTGTCAGAGAGATTAACATGATGATTTCTGACAGAGAG 1200
QY 1438 CAACATGATTAATTTGATCATCATGATTAATTTGCTGAGAGAGAGAGAGAGAGAGAGAGAG 1497
DB 1201 CAACATGATTAATTTGATCATCATGATTAATTTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAG 1260
QY 1498 CACCCAAATTCAGAGCTTGCATTAATTTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1557
DB 1261 CACCCAAATTCAGAGCTTGCATTAATTTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1320
QY 1558 TATGTCGGGAAACATTAAGAGCTGGCAAGTATGAGAGAGATTAACCCGAAATAGTGTGCT 1617
DB 1321 TATGTCGGGAAACATTAAGAGCTGGCAAGTATGAGAGAGATTAACCCGAAATAGTGTGCT 1380
QY 1618 ACCGTACCAATTAATGAGATGTTGGGGGATTTCACTGTAACCGAGAGAGAGAGAGAGAGAG 1677
DB 1381 ACCGTACCAATTAATGAGATGTTGGGGGATTTCACTGTAACCGAGAGAGAGAGAGAGAGAG 1440
QY 1678 GTTTGGGTGAAGCA 1692
DB 1441 GTTTGGGTGAAGCA 1455

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RESULT 12
ABLS0564
ID ABL50564 standard; DNA; 1455 BP.
XX
XX ABL50564;
XX
DT 19-JUN-2002 (first entry)

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XX DE Bacillus termamyl-like alpha-amylase encoding DNA SEQ ID NO:1.
XX
XX KW Bacillus; termamyl-like alpha-amylase; alpha-amylase; EC 3.2.1.1;
XX KM variant; mutant; enzyme; protein co-ordinate data; cleaning; detergent;
XX washing; sweetener; ethanol; starch; gene; ds.
XX OS Bacillus sp.
XX
XX FH Key Location/Qualifiers
XX CDS 1..1455
XX FT /*tag= a
XX FT /partial
XX FT /EC number= "3.2.1.1"
XX FT /product= "termamyl-like alpha-amylase"
XX FT /note= "no start or stop codons given"
XX
XX PN WO200166712-A2.
XX
XX PD 13-SEP-2001.
XX
XX PF 07-MAR-2001; 2001WO-DK000144.
XX
XX PR 08-MAR-2000; 2000DK-00000376.
XX PR 15-MAR-2000; 2000US-0189857P.
XX PR 23-FEB-2001; 2001DK-00000303.
XX PR 26-FEB-2001; 2001US-0271382P.
XX
XX PA (NOVO) NOVOZYMES AS.
XX
XX PI Andersen C, Borchert TV, Nielsen BR;
XX
XX DR MPI; 2002-239612/29.
XX
XX DR P-PSDB; ABE06933.
XX
XX PT Novel variant of parent termamyl-like alpha-amylase useful as a component
XX PT in washing and dishwashing compositions, for textile desizing, for starch
XX PT liquefaction, and for producing sweeteners and ethanol from starch.
XX
XX PS Disclosure; Page 130-131; 153pp; English.
XX
XX
XX CC The present invention describes a variant of a parent termamyl-like alpha
XX CC -amylase (EC 3.2.1.1) (I) comprising an alteration at one or more
XX CC positions of a group of 31 possible amino acid positions. The alteration
XX CC in (I) may be at Arg28, Arg118, Arg181, Gly182, Asp183, Gly184,
XX CC Gly186, Trp189, Asn195, Met202, Tyr298, Asn299, Lys302, Ser303, Asn306,
XX CC Arg310, Asn314, Arg320, His324, Glu345, Tyr396, Arg400, Trp439, Arg444,
XX CC Asn445, Lys446, Glu449, Arg458, Asn471, or Asn484. (I) can be used for
XX CC washing and/or dishwashing, textile desizing, and starch liquefaction.
XX CC (I) is useful as a component in hard surface cleaning detergent
XX CC composition, and for producing sweeteners and ethanol from starch. (I)
XX CC has altered solubility, preferably increased solubility, in particular
XX CC under washing, dish washing or hard surface cleaning conditions. The
XX CC present sequence encodes a Bacillus termamyl-like alpha-amylase which is
XX CC used in the exemplification of the present invention
XX
XX SQ Sequence 1455 BP; 461 A; 248 C; 361 G; 385 T; 0 U; 0 Other;
XX
XX
XX QY Query Match 65.7%; Score 1167; DB 6; Length 1455;
XX Best Local Similarity 87.6%; Pred. No. 2.5e-307;
XX Matches 1275; Conservative 0; Mismatches 180; Indels 0; Gaps 0;
XX
XX DB 1 CATCATTAATGGAACAAATGGTACTATGAGCAATATTTGAAATGATTTGCAAAATGAC 60
XX
XX QY 238 CATCATTAATGGAACAAATGGTACTATGAGCAATATTTGAAATGATTTGCAAAATGAC 297
XX
XX DB 298 GGAACCACTGGAACAGTTACGAGTACGAGCTTAATTAAGATTAAGAGGATTAAC 357
XX
XX DB 61 GGAATCATTTGGAACAGTTGAGGATGACGAGCTTAATTAAGATTAAGAGGATTAAC 120
XX
XX QY 358 GCTGTTGATTCCTCTGTCATGAGAGGGGACTTGCAGAAATGATGTTGGGTATGCTGCC 417
XX
XX DB 121 GCTGATATGATCCACCTTCATGAGAGGGGACTTGCAGAAATGATGTTAGTATGAGAGCC 180

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Qy 418 TATGATTGTACGATCTTGTGATGTTTAAACCAAAAGGAAACCGTCCGTAACAATATATGAC 477
 Db 181 TATGATTGTATGATCTTGTGAGATTTTACCAAGAAAGGAGCGTTCCGTAACAATATATGGA 240
 Qy 478 ACAAGAGTCAGTTGCAAGGTGCGGTGACATCTTTGAAAAATTAACGGGATTCAGATTAT 537
 Db 241 ACAAGCAACGATACAGGCTGCGGTGACCTTTTAAAAAATTAACGGGATTCAGATTAT 300
 Qy 538 GGGGATGTCGTGATGATCATTAAGGTGAGACACAGGAGACAGATGTGTAATGCGGTG 597
 Db 301 GGTATGTGCTGATGAATCATTAAGGTGAGACAGATGTGTAAGTAATGTAATGCGGTA 360
 Qy 598 GAAGTGAACCGAGACCAACCGAAACCAAGAAATATCAGGTGAATCACCATGGAAGCATGG 657
 Db 361 GAAGTGAATCGAGACCAACCGAAACCAAGAAATATCAGAGAGGTATGCAATGAAAGCGTGG 420
 Qy 658 ACGAAATTTGATTTCCCTGGAAGAGAAATACCATTCACATCTTAAATGGCGCTGTAT 717
 Db 421 ACAAGTTTGTATTTCTCGAAGAGAAATTAACCATTCACATCTTAAAGTGGCGCTGTAT 480
 Qy 718 CATTTTGTATGGGACAGATGGGATCAGTCAGCTCAGACCTTCGAACAAATATATTAATTC 777
 Db 481 CATTTTGTATGGGACAGATGGGATCAGTCAGCTCAGACCTTCGAACAAATATATTAATTC 540
 Qy 778 AGAGGTACCGGAAAGGACATGGGACATGGGAGTAGATATAGAGAACGGCACTATGATTAC 837
 Db 541 AGGGAACAGGACAGGCTGGGACCTGGGAGTCCATACAGAGAAATGGCACTTATGACTAT 600
 Qy 838 CTATATGATGACAGCATTTGATATGATATCAGAGATGATCAATCAATGAACTTAAAGATTTG 897
 Db 601 CTATATGATGACAGCATTTGATATGATATCAGAGATGATCAATCAATGAACTTAAAGATTTG 660
 Qy 898 GGAATTTGGTATACAAATACCTTAATCTAGATGATGATTAAGATCGATGCTGAACAT 957
 Db 661 GGAATTTGGTATACAAATACCTTAATCTAGATGATGATTAAGATCGATGCTGAACAT 720
 Qy 958 ATTAAATACAGCTATACAGAGATTTGGCTAACAGATGGCTAACACCAAGGTAAACCA 1017
 Db 721 ATTAAATACAGCTATACAGAGATTTGGCTTAACAGATGGCTTAACACCAAGGTAAACCA 780
 Qy 1018 ATGTTTCAGTTGACAGATTTTGGAAAAATGACCTTGCCTGCAATGCAAACTATTTAAAT 1077
 Db 781 ATGTTTCAGTTGACAGATTTTGGAAAAATGACCTTGCCTGCAATGCAAACTATTTAAAT 840
 Qy 1078 AAAACAAGTTGGAATCACTCCGTGTGATGATGCTCTTCATTAATTTGTACATGCA 1137
 Db 841 AAAACAAGTTGGAATCACTCCGTGTGATGATGCTCTTCATTAATTTGTACATGCA 900
 Qy 1138 TCTAATAGTGTGCTATTTTGTATATGAGAAATTTTAAATGTTCTGTCTGTAACAAA 1197
 Db 901 TCTAATAGTGTGCTATTTTGTATATGAGAAATTTTAAATGTTCTGTCTGTAACAAA 960
 Qy 1198 CACCTTATACATGACATCACTTTGTGATTAACCATGACTCTCAGCCAGAGAAACATTTG 1257
 Db 961 CATCAACACATGACCTTACTTTGTGATTAACCATGACTCTCAGCCAGAGAAACATTTG 1020
 Qy 1258 GAATCTTTTGTCAATCGTGTGTAACCACTGTCATATGATGATTTGTCAAGGAGAG 1317
 Db 1021 GAATCTTTTGTCAATCGTGTGTAACCACTGTCATATGATGATTTGTCAAGGAGAA 1080
 Qy 1318 CAAGGTTACCTTCCGATTTTAAAGGTATACCTATACCTGTAACCACTCATGTTCTT 1377
 Db 1081 CAAGGTTATCTTCCGATTTTAAAGGTATACCTATACCTGTAACCACTCATGTTCTTCCG 1140
 Qy 1378 TCGATGAATCTAAATATGATCACTTCTGAGGACAGTCAAGATATGCTTACGGAAC 1437
 Db 1441 GCTATGAATCTAAATATGATCACTTCTGAGGACAGTCAAGATATGCTTACGGAAC 1200
 Qy 1438 CAACATGATATTTTGTATCATATGATATTAATCGCTGAGACAGAGAGGGAACGCTCC 1497
 Db 1201 CAGCATGATATCTTTGTATCATATGATATTAATCGCTGAGACAGAGAGGGAATAGCTCC 1260

Qy 1498 CACCAAAATTCAGACCTTGCACTATTATGTCCGATGGGCGAGGGGTAATAATGATG 1557
 Db 1261 CATCAAAATTCAGGCTTGCCACCATTAATGTCAATGCTCAGGTGGTAACAATGATG 1320
 Qy 1558 TATGTGGGAAACATTAAGCTGGCCAAATATGAGATATTCACCGGAATATGCTCTGCT 1617
 Db 1321 TATGTGGGAAACATTAAGCTGGCCAAATATGAGATATTCACCGGAATATGAGACAGG 1380
 Qy 1618 ACCGTCACTTAATGAGATGTTGGGGAATTTCACTGTAAACGAGAGGCGAGTTTCG 1677
 Db 1381 ACCGTCACTTAATGAGATGTTGGGGAATTTCTGTATATGAGAGGCTCCGTTTCG 1440
 Qy 1678 GTTTGGGTGAAGCA 1692
 Db 1441 GTTTGGGTGAAGCA 1455

RESULT 13
 AAS20022
 ID AAS20022 standard; DNA; 1455 BP.
 XX
 AC AAS20022;
 XX
 DT 09-APR-2002 (first entry)
 XX
 DE Bacillus DNA encoding TERMAMYL-like alpha-amylose SP690.
 XX
 KW TERMAMYL; alpha-amylose; ds; detergent; dishwashing; textile desizing;
 KW starch liquefaction; ethanol production; hard surface cleaner; sweetener;
 KW amylopectin; limit dextrin; NOVAMYL; SP690.
 OS Bacillus sp.
 XX
 FH Key Location/Qualifiers
 FT 1. 1455
 FT CDS /*tag= a
 FT /*product= "Alpha-amylose SP690"
 FT /*partial
 FT /*note= "No start or stop codon"
 XX
 XX MO20018107-A2.
 XX
 PD 22-NOV-2001.
 XX
 PF 10-MAY-2001; 2001MO-DK000323.
 XX
 PR 12-MAY-2000; 2000DK-00000779.
 XX
 PA (NOVO) NOVOZYMES AS.
 XX
 PI Svendsen A, Jorgensen CT, Nielsen BR;
 XX
 DR WPI; 2002-106123/14.
 XX
 PS P-PSDB; AAU12149.
 XX
 PT New variant of parent Termamy1-like alpha-amylose for use as a component
 PT in washing and dishwashing compositions, for textile desizing, for starch
 PT liquefaction, and for producing sweeteners and ethanol from starch.
 XX
 PS Disclosure; Page 42-45; 84pp; English.
 XX
 CC The invention relates to a variant of parent TERMAMYL-like alpha-amylose
 CC comprising an alteration at regions 186-193, 261-276, 283-293 or 334-339,
 CC or at position 234, where the variant has alpha-amylose activity and each
 CC position corresponds to a position of a parent Termamy1-like alpha-
 CC amylose sequence having a Bacillus licheniformis alpha-amylose sequence
 CC of 483 amino acids, given in specification. The variant alpha-amylose, a
 CC detergent additive comprising the variant or a detergent composition
 CC comprising the variant, is useful for washing and/or dishwashing or
 CC textile desizing. The alpha-amylose is useful for starch liquefaction or
 CC ethanol production and as a component in a hard surface cleaning
 CC detergent composition, and for producing sweeteners from starch. The
 CC variant has altered alpha-1, 6-D-glucosidic branch linkage cleavage

CC activity on amylopectin, preferably increased alpha-1, 6-D-glucosidic
 CC branch linkage cleavage activity of amylopectin or a limit dextrin
 CC prepared by TERMAMYL (R)M or NOVAMYL (R)M. The present sequence encodes
 CC a natural variant of the TERMAMYL alpha-amylase, Sp690
 CC XX

Sequence 1455 BP; 461 A; 248 C; 361 G; 385 T; 0 U; 0 Other;

Query Match 65.7%; Score 1167; DB 6; Length 1455;
 Best Local Similarity 87.6%; Pred. No. 2.5e-307;
 Matches 1275; Conservative 0; Mismatches 180; Indels 0; Gaps 0;

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QY 238 CATCAATAAGGAGCAGATGGAGCCATGATGAGTATTTGAATGAGCATTTGCCAATGAC 297
DB 1 CATCAATAAGGAGCAGATGGAGCCATGATGAGTATTTGAATGAGCATTTGCCAATGAC 60
QY 298 GGGAGCACTGGAGACAGTTAGAGATGACGCGTAACTTAAAGATTAAGGATACC 357
DB 61 GGGAGCACTGGAGACAGTTAGAGATGACGCGTAACTTAAAGATTAAGGATTAAGCA 120
QY 358 GCGTTTGGATTCCCTGATGAGAGGGGACTTGGCAAAATGATGTTGGTATGTTGCC 417
DB 121 GCGTATGAGATCCCATGATGAGAGGGGACTTCCAGATGATGATGATTAAGAGCC 180
QY 418 TATGATTTGATGATCTTGGTGAATTTAAACCAAGAGGAAACCGTCCGTACAAATATGCG 477
DB 181 TATGATTTATATGATCTTGGAGAGTTTAAACCAAGAGGAGCGGTGCTACAAATATGGA 240
QY 478 ACAAGAGATCAGTTGCAAGTGCCCGTCAATCTTTGAAATAACGGGATTCAGTTTAT 537
DB 241 ACAAGAGATCAGTTGCAAGTGCCCGTCAATCTTTGAAATAACGGGATTCAGTTTAT 300
QY 538 GGGAGTGTGCTGATGATCAATAAGGTGAGCAGAGCGGACAGAGATGTAATGCGGTG 597
DB 301 GGGAGTGTGCTGATGATCAATAAGGTGAGCAGAGCGGATGTAATGTAATGCGGTG 360
QY 598 GAAGTGAACCGAAGCAACCGAAACCAAGAAATATCAGTGAATATACCAATTGAAGCATG 657
DB 361 GAAGTGAATCGAGCAACCGAAACCAAGAAACCTCAGAGATATCAATATGAAGCGGTG 420
QY 658 AGCAATTTGATTTCCCTGGAAGAGAAATACCATTTCCCACTTTAAATGCGCTGTAT 717
DB 421 ACMAATTTGATTTCCCTGGAAGAGAAATATACCATTTCCCACTTTAAATGCGCTGTAT 480
QY 718 CATTTGATGGGACAGATTTGGGATCGTCACTGCTGATGAGCAACAAATATATTAATTC 777
DB 481 CATTTGATGGGACAGATTTGGGATCGTCACTGCTGATGAGCAACAAATATATTAATTC 540
QY 778 AGAGTACCGGAAGGATGGAATGGAAGTATGATATAGAGAACGGCAATATATGATTAC 837
DB 541 AGGGGAACAGGCAAGGCTGGGATCGGGAAGTCAATACAGAGATGGAATATATGACTAT 600
QY 838 CTATATGATGACACATTTGATATGATCATCCGAAAGTATCAATGAATCTTAAGAAATGG 897
DB 601 CTATATGATGACACATTTGATATGATCATCCGAAAGTATATCAATGAATCTTAAGAAATGG 660
QY 898 GGAGTTTGGATATCAATATACCTTAATCTAGATGATTTAGATTCATGCTGTGAACAT 957
DB 661 GGAGTGTGATATCAATATACCTTAATCTAGATGATTTAGATTCATGCTGTGAACAT 720
QY 958 ATTAAATACAGCTATACGAGAGATTTGCTTAACATATGCTGTAACCAACAGGTAAACCA 1017
DB 721 ATTAAATATATGCTTATACGAGAGATTTGCTTAACATATGCTGTAACCAACAGGTAAACCA 780
QY 1018 ATGTTTGGAGTTGCAAAATTTTGGAAATATGACCTTGTGCAATTCGAAATCTTTAAAT 1077
DB 781 ATGTTTGGAGTTGCTATGATTTTGGAAATATGACCTTGTGCAATTTGAAATCTTTAAAT 840
QY 1078 AAAACAAGTTGATCACTCCGTTGATGATGTTCTCTTCATATATATTTGATCAATGCA 1137
DB 841 AAAACAAGTTGATCACTCCGTTGATGATGTTCTCTCTCCATATATTTTGTATCAATGCA 900
QY 1138 TCTAATATGTTGTTGCTATTTTGAATATGAGAAATATTTTAAATGTTCTGTGTAACAAA 1197

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DB 901 TCTAATATGTTGTTATTTATGATATGAGAAATATTTTAAATGTTCTGTGTAACAAA 960
QY 1198 CACCTATATACATGATGATCAATTTTGTATATACCAATGATCTCCAGCCAGGAGAACATTTG 1257
DB 961 CATCCAAACATGATGATGATCTTTTGTATATACCAATGATCTCCAGCCAGGAGAACATTTG 1020
QY 1258 GAATCCTTTGTTCAATCGTGTTCAACACATGCAATATGATGATTTCTGCAAGGAG 1317
DB 1021 GAATCCTTTGTTCAATCGTGTTCAACACATGCAATATGATGATTTCTGCAAGGAG 1080
QY 1318 CAAGTTTACCTTCCGATATTTTACGATATTAATAAGTATACCAATCTCATGTTCTCT 1377
DB 1081 CAAGTTTACCTTCCGATATTTTATGAGGATTAATAAGTATACCAATCTCATGTTCTCT 1140
QY 1378 TCGATGAATCTTAAATGATATCACTTTCGAGGAGACGCAACGTAATGCTTACGGAACC 1437
DB 1141 GCTATGAATCTTAAATGATATCACTTTCGAGGAGACGCAACGTAATGCTTACGGAACC 1200
QY 1438 CAACATGATTTTATGATCATGATATATATCGCTGAGACGAGAGAGGAGACGCTCC 1497
DB 1201 CAGCATGATTTATTTGATGATCATGATATATATCGGTTGACAAAGAGAGAAATAGCTCC 1260
QY 1498 CACCAATTCAGACTTGCAATTAATATGATGCTGATGCGCCAGGGGTTAATATGATG 1557
DB 1261 CATCAAAATTCAGGCTTGCCACATTAATGATGATGATGATGATGATGATGATGATG 1320
QY 1558 TATGTCGGGAAACATTAAGCTGCGCAAGTATGAGAGATATACCGGAAATAGGTCTG 1617
DB 1321 TATGTCGGGAAACATTAAGCTGCGCAAGTATGAGAGATATTAACGGAAATAGGACAGGC 1380
QY 1618 ACCGTCAACATTAATGATGATGTTGGGGAATTTCACTGTAACGAGAGGACAGTTTCG 1677
DB 1381 ACCGTCAACATTAATGATGATGTTGGGGAATTTCACTGTAATGAGAGGACAGTTTCG 1440
QY 1678 GTTTGGTGAACCA 1692
DB 1441 GTTTGGTGAACCA 1455

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RESULT 14

AA172211
 ID AA172211 standard; cDNA; 1455 BP.

XX AA172211;

DT 02-APR-2002 (first entry)

XX Bacillus alpha amylase sp690 cDNA.

DE Alpha amylase; Bacillus; Termamyl-1like; maltodextrin; glucose syrup;

KW starch; food; feed; pharmaceutical; confectionery; candy; isotonic drink;

KW bakery; cereal bar; ice cream; coffee whitener; salad dressing;

KW cured meat; fermented meat; spice; ss.

XX Bacillus sp.

OS Key Location/Qualifiers

FT CDS 1.1455

FT /tag= a

FT /note= "No stop codon given"

PN MO200196537-A2.

PD 20-DEC-2001.

XX 13-JUN-2001; 2001WO-DK000404.

XX 14-JUN-2000; 2000DK-0000917.

PR 20-JUN-2000; 2000US-0212852P.

XX (NOVO) NOVOZYMES AS.

PA Nielsen BR, Weibye M;

PI

XX WPI: 2002-098064/13.
 DR P-PSDB: AAB47850.
 XX New modified alpha-amylase derived from the genus *Bacillus* and/or is a
 PT Teramyl-1-like alpha-amylase, which has been pre-oxidized for producing
 PT maltodextrin or glucose syrup.
 XX
 PS Claim 7; Page 23-25; 47pp; English.
 XX
 The sequences given in A1172211-16 encode modified alpha-amylases derived
 CC from the genus *Bacillus*. These alpha amylases are Teramyl-1-like alpha-
 CC amylase and they have been pre-oxidized. The alpha amylase is useful for
 CC producing a maltodextrin or glucose syrup, by treating starch with a pre-
 CC oxidized alpha-amylase until a product with a DE between 5-45 has been
 CC provided and/or until a product with a molecular weight of between 5-30
 CC kDa has been provided. The product comprises a maltodextrin with a DE of
 CC 18.5 and/or a maltodextrin with a molecular weight of 14-16 kDa. The
 CC alpha amylase is useful for producing a maltodextrin or glucose syrup,
 CC where the glucose syrup is useful as an ingredient in food, feed or
 CC pharmaceuticals. Glucose syrup is useful in confectionery such as
 CC candies, beverages such as isotonic drinks, bakery such as cereal bars,
 CC dairy and ice cream such as coffee whiteners, conventional foods such as
 CC salad dressings, meat, and food ingredients and preparations such as cured
 CC meat, fermented meat, spices and seasoning encapsulated flavours
 XX
 Sequence 1455 BP; 461 A; 248 C; 361 G; 385 T; 0 U; 0 Other;
 Query Match 65.7%; Score 1167; DB 6; Length 1455;
 Best Local Similarity 87.6%; Pred. No. 2,5e-307;
 Matches 1275; Conservative 0; Mismatches 180; Indels 0; Gaps 0;

DB CTTATGATGACAGCGTGATATGATGATCACCAGAGTAATATGAACTGAACTGG 660
 QY 898 GGAGTTGGTATPACAAATATACCTTAATCTAGATGATTTAGAAATGATGCTGTGAAACAT 957
 DB 661 GGAGTGGTATPACAAATATACCTTAATCTAGATGATTTAGAAATGATGCTGTGAAACAT 720
 QY 958 ATTAATATACCTTAATPACAGAGATTTGGCTAACATGAGCTTAACACCAAGGTAAACCA 1017
 DB 721 ATTAATATPACCTTTACAGAGATTTGGCTTAACATGCTTAACACCAAGGTAAACCA 780
 QY 1018 ATGTTGACGTGACGATTTTGGAAATATGACCTTGTGCAATGCAAACTATTTAAAT 1077
 DB 781 ATGTTGACGAGGTGATTTTGGAAATATGACCTTGTGCAATGCAAACTATTTGAT 840
 QY 1078 AAAACAGTTGGAATCACTCCGTGTGATGATTTCTCTTCAATTAATTTGATGACCA 1137
 DB 841 AAAACAGTTGGAATCACTCCGTGTGATGATTTCTCTTCAATTAATTTGATGACCA 900
 QY 1138 TCTAATATGCTGCTATTTTGAATATGAGAAATATTTAAATGTTCTGTGTAACAAA 1197
 DB 901 TCTAATATGCTGCTATTTATGATATGAGAAATATTTAAATGTTCTGTGTAACAAA 960
 QY 1198 CACCTTATACATGACATGACATTTGTTGATPACCATGACTCTCAGCCAGAGAAACATTTG 1257
 DB 961 CATCAACACATGCTGCTATCTTTGTTGATPACCATGACTCTCAGCCAGAGAAACATTTG 1020
 QY 1258 GAATCTTTGTTCAATGCTGCTCAAAACACTGSCATATGATGATTTGCAAGAGAG 1317
 DB 1021 GAATCTTTGTTCAATGCTGCTCAAAACACTGSCATATGATGATTTGCAAGAGAG 1080
 QY 1318 CAAGTTATCCTTCGTAATTTATGAGGATTAATGAGGATTAATGAGGATTAATGAGG 1377
 DB 1081 CAAGTTATCCTTCGTAATTTATGAGGATTAATGAGGATTAATGAGGATTAATGAGG 1140
 QY 1378 TCGATGAATATTAATATGATGATCACTCTGCAAGCACTCAAGATATGCTTACGAAAC 1437
 DB 1141 GCTATGAATATTAATATGATGATCACTCTGCAAGCACTCAAGATATGCTTACGAAAC 1200
 QY 1438 CAACATGATTTATTTGATCATGATATTTATGAGGCTGAGAGAGAAAGGAGCAAGCTCC 1497
 DB 1201 CAGCATGATTTATTTGATCATGATATTTATGAGGCTGAGAGAGAAAGGAGCAAGCTCC 1260
 QY 1498 CACCAATTTAGAGATTTGCACTTATTTATGCTGCAATGAGGCTGAGAGAGAAAGGAG 1557
 DB 1261 CATCAAAATTCAGCTGCTGCACTTATTTATGCTGCAATGAGGCTGAGAGAGAAAGGAG 1320
 QY 1558 TATGTCGAGAAACATTAAGCTGAGCAAGTATGAGAGATATCAACGAAATAGGCTGCT 1617
 DB 1321 TATGTCGAGAAACATTAAGCTGAGCAAGTATGAGAGATATCAACGAAATAGGCTGCT 1380
 QY 1618 ACCGTACCATTAATGAGATGTTGGGGAATTTCACTGTAAACGAGGGGAGATTTG 1677
 DB 1381 ACCGTACCATTAATGAGATGTTGGGGAATTTCACTGTGTAAATGAGGGTCCGTTTCG 1440
 QY 1678 GTTGGGTGAAGCA 1692
 DB 1441 GTTGGGTGAAGCA 1455

RESULT 15
 ABL96207
 ID ABL96207 standard; DNA; 1455 BP.
 XX ABL96207;
 AC
 XX
 DT 19-AUG-2002 (first entry)
 XX
 XX Teramyl-1-like-alpha-amylase encoding sequence #1.
 DE Teramyl-1: alpha amylase; starch liquefaction; ethanol production;
 XX textile desizing; detergent; enzyme; gene; ds.
 XX

OS Bacillus sp.
 XX Key Location/Qualifiers
 FT CDS 1..1455
 FT /tag= a
 FT /product= "termyl-like alpha amylase"
 FT /partial
 FT /note= "no start or stop codon"
 XX
 XX MO200210355-A2.
 XX
 XX 07-FEB-2002.
 XX
 XX 12-JUL-2001; 2001MO-DK000488.
 XX
 XX 01-AUG-2000; 2000DK-00001160.
 XX
 XX 12-SEP-2000; 2000DK-00001354.
 XX
 XX 10-NOV-2000; 2000DK-00001687.
 XX
 XX 26-APR-2001; 2001DK-00000655.
 XX
 XX (NOVO) NOVOZYMES AS.
 XX
 XX Thisted T, Kjaerulff S, Andersen C, Fuglsang CC;
 XX
 XX WPI; 2002-280633/32.
 XX
 XX P-PSDB; ABB76586.
 XX
 XX Variant of parent Termamy]-like alpha amylase, useful in detergent
 XX compositions, for starch liquefaction, ethanol production, washing and/or
 XX dish washing, and textile desizing.
 XX
 XX Disclosure; Page 55-57; 90pp; English.
 XX
 XX This invention relates to variants of a parent Termamy]-like alpha-
 XX amylases. These are used for starch liquefaction, ethanol production,
 XX detergent, and textile desizing. The amylases have altered stability,
 XX particularly at high temperatures from 70-120plusoc and low pH in the
 XX range from pH 4.0-6.0. The present sequence is a termamy]-like-alpha-
 XX amylase encoding sequence
 XX
 XX Sequence 1455 BP; 461 A; 248 C; 361 G; 385 T; 0 U; 0 Other;
 XX
 XX Query Match 65.7%; Score 1167; DB 6; Length 1455;
 XX Best Local Similarity 87.6%; Pred. No. 2.5e-307;
 XX Matches 1275; Conservative 0; Mismatches 180; Indels 0; Gaps 0;
 XX
 XX 238 CATCATATATGGAGCAATGGGACCATGATGAGTATTTGATGCAATTTGCCAAATGAC 297
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OM nucleic - nucleic search, using sw model

Run on: May 2, 2005, 17:25:37 ; Search time 227 Seconds

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Gapop 10.0, Gapext 1.0

Searched: 1202784 seqs, 81813359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

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; Sequence 1, Application US/09986676A
; Patent No. 6638748
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GENERAL INFORMATION:
; APPLICANT: HATADA, Yuji
; APPLICANT: OZAKI, Katsuya
; APPLICANT: ARA, Katsutoshi
; APPLICANT: KAWAI, Shuji
; APPLICANT: ITO, Susumu
;
TITLE OF INVENTION: Gene Encoding Alkaline Liquefying Alpha-Amylase
;
FILE REFERENCE: 2173-0121P
;
CURRENT APPLICATION NUMBER: US/09/986,676A
;
PRIOR FILING DATE: 2001-11-09
;
PRIOR APPLICATION NUMBER: PCT/JP96/01641
;
PRIOR FILING DATE: 1996-06-14
;
PRIOR APPLICATION NUMBER: Japan 147257/1995
;
NUMBER OF SEQ ID NOS: 12
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SOFTWARE: PatentIn version 3.1
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SEQ ID NO 1
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LENGTH: 1776
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TYPE: DNA
;
ORGANISM: Bacillus sp.
;
FEATURE:
; NAME/KEY: CDS
; LOCATION: (145)..(1692)
; OTHER INFORMATION:
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 1776; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Solicitation HHS/09971611

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2      Patent No. 6743616
3      GENERAL INFORMATION:
4      APPLICANT: ARAKI, HIROYUKI
5      APPLICANT: ENDO, KEIJI
6      APPLICANT: HAGIHARA, HIROSHI
7      APPLICANT: IGARASHI, KAZUKI
8      APPLICANT: HAYASHI, YASUHIRO
9      APPLICANT: OZAKI, KATSUYA
10     TITLE OF INVENTION: HIGHLY PRODUCTIVE ALPHA-AMYLASES
11     FILE REFERENCE: 214377US0
12     CURRENT APPLICATION NUMBER: US/09/971,611
13     CURRENT FILING DATE: 2001-10-09
14     PRIOR APPLICATION NUMBER: JP 2000/310605
15     PRIOR FILING DATE: 2001-10-11
16     NUMBER OF SEQ ID NOS: 51
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27     LOCATION: (248)..( )
28     OTHER INFORMATION:
29     NAME/KEY: CDS
30     LOCATION: (155)..(1702)
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32     US-09-971-611-1

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 Db 1571 GTCCGGAACATTAAGTGGCCAAATGAGATGAGATATCACCGGAATATGCTGTGATCC 1630
 Qy 1621 GTCAACATTAATGAGATGTTGGGGAAATTTCACTGTAAACGAGGGGCACTTCGCTT 1680
 Db 1631 GTCAACATTAATGAGATGTTGGGGAAATTTCACTGTAAACGAGGGGCACTTCGCTT 1690
 Qy 1681 TGGGTGAAGCAATTAATTAAGGAACAAGAGGGGAAATTAATCTTCTCATACAGAGCTT 1740
 Db 1691 TGGGTGAAGCAATTAATTAAGGAACAAGAGGGGAAATTAATCTTCTCATACAGAGCTT 1750
 Qy 1741 CCGATCACTCATACACCAATATTAATTTGAAGCTT 1776
 Db 1751 CCGATCACTCATACACCAATATTAATTTGAAGCTT 1786

RESULT 3
 US-08-600-908A-11
 ; Sequence 11, Application US/08600908A
 ; Patent No. 5989169
 ; GENERAL INFORMATION:
 ; APPLICANT: Svendsen, Allan
 ; APPLICANT: Bisg rd-Frantzen, Henrik
 ; APPLICANT: Borchert, Torben Vedel
 ; TITLE OF INVENTION: "-Amylase Mutants
 ; NUMBER OF SEQUENCES: 13
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESS: No. 59891690 No. 5989169disk of No. 5989169th America, Inc.
 ; STREET: 405 Lexington Avenue, 64th Floor
 ; CITY: New York
 ; STATE: New York
 ; COUNTRY: United States of America
 ; ZIP: 10174-6401
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/600,908A
 ; FILING DATE: 13-FEB-1996
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:

NAME: Green, Reza
 REGISTRATION NUMBER: 38,475
 REFERENCE/DOCKET NUMBER: 4394.204-US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 212-867-0123
 TELEFAX: 212-878-9655
 INFORMATION FOR SEQ ID NO: 11:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1458 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 1..1455
 US-08-600-908A-11

Query Match 65.9%; Score 1170; DB 2; Length 1458;
 Best Local Similarity 87.7%; Pred. No. 0;
 Matches 1278; Conservative 0; Mismatches 180; Indels 0; Gaps 0;

QY 238 CATCATATATGGAAGGATGGGACCATGATGACAGTATTTGAAATGGCATTTGCCAAATGAC 297
 DB 1 CATCATATATGGAAGGATGGGACCATGATGACAGTATTTGAAATGGCATTTGCCAAATGAC 60
 QY 298 GGGAAACACTGGAAACAGTTACGAGATGACGCGCTAATCTTAAAGATTAAGGATTTACC 357
 DB 61 GGGAAACACTGGAAACAGTTACGAGATGACGCGCTAATCTTAAAGATTAAGGATTTACC 120
 QY 358 GCTGTTTGATTCCTCTGTCGATGAAAGGGGACTTCCGAAATGATGTTGGGTATGGTGC 417
 DB 121 GCTGTTTGATTCCTCTGTCGATGAAAGGGGACTTCCGAAATGATGTTGGGTATGGTGC 180
 QY 418 TATGATTTGATGATCTTGGTGAAGTTTAAACCAAAAGGAAACCGTCCGTAACAAATATGAC 477
 DB 181 TATGATTTGATGATCTTGGTGAAGTTTAAACCAAAAGGAAACCGTCCGTAACAAATATGAC 240
 QY 478 ACAAGAGTCAGTGGCAAGTGCCTGATCATCTTTGAAATTAACGGATTCAGTTTAT 537
 DB 241 ACAAGAGTCAGTGGCAAGTGCCTGATCATCTTTGAAATTAACGGATTCAGTTTAT 300
 QY 538 GGGGATGTCGTGATGATCATTAAGGTGAGCAGACGGGACAGAGATGTTAAATGGCGTG 597
 DB 301 GGGGATGTCGTGATGATCATTAAGGTGAGCAGACGGGACAGAGATGTTAAATGGCGTG 360
 QY 598 GAAGTGAACCGAAGCAACCGAAACCAAGAAATATCAGTGAATATCACCATTTAAGCATG 657
 DB 361 GAAGTGAACCGAAGCAACCGAAACCAAGAAATATCAGTGAATATCACCATTTAAGCATG 420
 QY 658 ACGAATTTGATTTCCCTGGAAGAGAAATACCATTTCCACTTTAAATGGCGCTGTAT 717
 DB 421 ACGAATTTGATTTCCCTGGAAGAGAAATACCATTTCCACTTTAAATGGCGCTGTAT 480
 QY 718 CATTGATGAGGACAGATTTGGGATCAGTCACGTCACTTACAGAAACAAATATATTAATTC 777
 DB 481 CATTGATGAGGACAGATTTGGGATCAGTCACGTCACTTACAGAAACAAATATATTAATTC 540
 QY 778 AGAGTACCGGAAGGATGGAACCTGGGAAGTATATAGAAACGCAACTATATGATTC 837
 DB 541 AGAGTACCGGAAGGATGGAACCTGGGAAGTATATAGAAACGCAACTATATGATTC 600
 QY 838 CTATATGATGACAACTGATATGATGATCATCCAGAAAGTATCATATGAACTTAATTTG 897
 DB 601 CTATATGATGACAACTGATATGATGATCATCCAGAAAGTATCATATGAACTTAATTTG 660
 QY 898 GGAGTTTGATTAACAATACCTTAATCTAGATGATTTGAAATGATGATGATGATGAT 957
 DB 661 GGAGTTTGATTAACAATACCTTAATCTAGATGATTTGAAATGATGATGATGATGATGAT 720
 QY 958 ATTAAATACAGTATACAGAGAGATTTGGCTTAACATATGCGTAAACCAAGGATTAACCA 1017
 DB 721 ATTAAATACAGTATACAGAGAGATTTGGCTTAACATATGCGTAAACCAAGGATTAACCA 780

QY 1018 ATGTTTGACGTTGCAAGATTTTGGAAATATGACCTTGCTGCAATGCAAAATATTTAAT 1077
 DB 781 ATGTTTGACGTTGCAAGATTTTGGAAATATGACCTTGCTGCAATGCAAAATATTTGAAT 840
 QY 1078 AAAACAAGTTGGAATCACTCCGCTGCTGATGATGTTCTCTTCAATTAATTTGTAACAATGCA 1137
 DB 841 AAAACAAGTTGGAATCACTCCGCTGCTGATGATGTTCTCTCTCAATTAATTTGTAACAATGCA 900
 QY 1138 TCTAATATGCTGCTGCTATTTTGAATATGAGAAATATTTTAAATGTTCTCTGTAACAAA 1197
 DB 901 TCTAATATGCTGCTGCTATTTTGAATATGAGAAATATTTTAAATGTTCTCTGTAACAAA 960
 QY 1198 CACCCATATCATGCTGCAATTTGTTGATTAACATATGATCTCAGCCAGAGAGATTTG 1257
 DB 961 CACCCATATCATGCTGCAATTTGTTGATTAACATATGATCTCAGCCAGAGAGATTTG 1020
 QY 1258 GAATCCTTTGTTCAATCGTGTTCACAAACCACTGCAATATGATGATTTCTGACAAAGGAG 1317
 DB 1021 GAATCCTTTGTTCAATCGTGTTCACAAACCACTGCAATATGATGATTTCTGACAAAGGAG 1080
 QY 1318 CAAGTTTACCTTCCGATATTTAAGGTATTAAGTATTAAGTATTAAGTATTAAGTATTAAG 1377
 DB 1081 CAAGTTTACCTTCCGATATTTAAGGTATTAAGTATTAAGTATTAAGTATTAAGTATTAAG 1140
 QY 1378 TCGATGAATCTTAAATGATGCACTTTCGAGGACGCTCAACGATGCTTACGGAAC 1437
 DB 1141 TCGATGAATCTTAAATGATGCACTTTCGAGGACGCTCAACGATGCTTACGGAAC 1200
 QY 1438 CAACATGATTAATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1497
 DB 1201 CAACATGATTAATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1260
 QY 1498 CACCCAAATTCAGACTTTCACATTAATGTCGATGATGATGATGATGATGATGATGATGATG 1557
 DB 1261 CACCCAAATTCAGACTTTCACATTAATGTCGATGATGATGATGATGATGATGATGATGATG 1320
 QY 1558 TATGTCGGGAAACATTAACCTGCAAGATGATGATGATGATGATGATGATGATGATGATG 1617
 DB 1321 TATGTCGGGAAACATTAACCTGCAAGATGATGATGATGATGATGATGATGATGATGATG 1380
 QY 1618 ACCGTACCATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1677
 DB 1381 ACCGTACCATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1440
 QY 1678 GTTGGGTGAAGCAATTA 1695
 DB 1441 GTTGGGTGAAGCAATTA 1458

RESULT 4
 US-08-683-838A-11
 ; Sequence 11, Application US/08683838A
 ; Patent No. 6022724
 ; GENERAL INFORMATION:
 ; APPLICANT: Svendsen, Allan
 ; APPLICANT: Bisg rd-Franzen, Henrik
 ; APPLICANT: Borchert, Torben Vedel
 ; TITLE OF INVENTION: "-Amylase Mutants
 ; NUMBER OF SEQUENCES: 13
 ; CORRESPONDENCE ADDRESSES:
 ; ADDRESS: No. 6022724 No. 6022724disk of No. 6022724th America, Inc.
 ; CITY: New York
 ; STATE: New York
 ; COUNTRY: United States of America
 ; ZIP: 10174-6401
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent in Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:


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1 APPLICATION NUMBER: US/08/600,656
2 FILING DATE: 13-FEB-1996
3 CLASSIFICATION: 435
4 ATTORNEY/AGENT INFORMATION:
5 NAME: Lambiris, Eliaas J.
6 REGISTRATION NUMBER: 33,128
7 REFERENCE/DOCKET NUMBER: 4318.204-US
8 TELECOMMUNICATION INFORMATION:
9 TELEPHONE: 212 867 0123
10 TELEFAX: 212 867 0298
11 INFORMATION FOR SEQ ID NO: 4:
12 SEQUENCE CHARACTERISTICS:
13 LENGTH: 1455 base pairs
14 TYPE: nucleic acid
15 STRANDEDNESS: single
16 TOPOLOGY: linear
17 MOLECULE TYPE: DNA (genomic)
18 US-08-600-656-4

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Query Match	65.7%	Score 1167	DB 3	Length 1455
Best Local Similarity	87.6%	Pred. No. 0		
Matches 1275	Conservative	0	Mismatches 180	Indels 0
			Gaps	0

Qy	238	CATCATATATGGGACCAATGGGACCAATGATGACGATATTTTGAATGGCATTTGGCAATATGAC	297
Db	1	CATCATATATGGAAACAATATGATCTATGATGCAATTTTCGATATGATTTTGGCAATATGAC	60
Qy	298	GGGAACCACTGGAACAGGTTACAGATGACGACGCTTAACCTTAAGAGTAAGGGATTAACC	357
Db	61	GGGAATCATTTGGAAACAGGTTGAGGATGACGACGCTTAACCTTAAGAGTAAGGGATTAACA	120
Qy	358	GCTGTTTGAGATTCCTCCCTGCATATGGAAGGGGAACTTCGCAAAATGATGGTGGGATATGATGCC	417
Db	121	GCTGTTATGATATCCCACTTCGATATGGAAGGGGAACTTCGCAAAATGATGGTGGGATATGATGCC	180
Qy	418	TATGATTTTGTACGATCTTGATGATTTTAACCAAAAGGAAACCGTCCGTACAAATATATGAC	477
Db	181	TATGATTTTATATGATCTTGAGAGTTTAAACGAAGGGGACGGTTTCGTACAAATATATGGA	240
Qy	478	ACAAAGAGTCAGTTTGCAGAGTGTCCTGTACATCTTTGAAAAAATATACGGGATTTCAAGTTAT	537
Db	241	ACAGCGCAACCAAGCTACAGGCTGCGGTGACCTCTTTAAAAAATATACGGGATTTCAAGTATAT	300
Qy	538	GGGATGTCGATGATGAATCATTAAGAGTGGAGACAGCGGGAACGATGGTAAATCGGGT	597
Db	301	GGTATGTCGTCATATGATCATTAAGAGTGGAGACAGATGGTACCGAAATTTGTATATCGGTA	360
Qy	598	GAAGTGAACCGAAGCAACCGAAACCAAGAAATATCAGGTGATACCACTTGAACATATG	657
Db	361	GAAGTGAATCGAGCAACCGAAACCGAAACCTCAGGAGATATGCAATATGAACGATGG	420
Qy	658	ACGAAATTTGATTTCCCTCGGAAGAGGAATATCCCTTTCCACTTTAAATGGCGCTGTAT	717
Db	421	ACAAAGTTTATTTTCTCTGGAAGAGGAATATACCTTTCAGGTTTAAAGTGGCGCTGTAT	480
Qy	718	CATTTTGTATGGACAGATTTGGGATCAGTCAAGTCAGTTTCAGAAACAATATATATAATTC	777
Db	481	CATTTTGTATGGGACAGATTTGGGATCAGTCAAGTCAGTTTCAGAAACAATATATATAATTC	540
Qy	778	AGAGGTATCCGAAAGGCATGGGACTGGGAAGTATGATATAGAAACGGCACTATGATTAAC	837
Db	541	AGGGGAACAGGCAAGGCTCTGGGACTGGGAAGTATGATATAGAAATGGCAACTATATATAT	600
Qy	838	CTTATGTATGACAGCATTTGATATGAGATATCATCAAGAAATATCAATGAACCTTAGAAATTTG	897
Db	601	CTTATGTATGACAGAGCTGATATGAGATATCAACCAAGAAATATATCAATGAACCTTAGAAATTTG	660
Qy	898	GGAGTTTGGTATCAAAATATACCTTATATATAGATGGATTTAGATGATGATGCTGTGAAACAT	957
Db	661	GGAGTTTGGTATATCAAAATATACCTTATATATAGATGGATTTAGATGATGATGCTGTGAAACAT	720
Qy	958	ATTAAATATACCTATATAGAGATTTGGTTACACATGTGCGTAACACACACAGATTAACCA	1017

Db	721	ATAAATAATACCTTACAGAGATTTGGCTTACACATGTCCTAAACACACAGTAAACA	780
QY	1018	ATGTTTGCAGTTGCAGAAATTTTGGAAAAATGACCTTGTGCAATCGAAACTATTATTAAT	1077
Db	781	ATGTTTGCAGTGGCTGGAGTTTGGAAAAATGACCTTGGTGCAAATGGAACCTAATTTGGAT	840
QY	1078	AAAACAAGTGGAAATCACTCCGCTGTGGATGTCCTCTCAATPAAATTTGTACAAATGCA	1137
Db	841	AAAACAAGTGGAAATCACTCCGCTGTGGATGTCCTCTCACTAATTTGTACAAATGCA	900
QY	1138	TCTAATAGTGGCTAATTTTGTATGATGAGAAATTTTAAATGCTGTGTGCAAAAA	1197
Db	901	TCTAATAGCGGTGGTATTATGATGATGAGAAATTTTAAATGCTGTGTGTGCAAAAA	960
QY	1198	CACCCCTATACATGCAGTCACTTTGTTGATPACCATGACTCTCAAGCAGAGAAACATTG	1257
Db	961	CATCCACACACAGCCGTTACTTTGTTGATPACCATGACTCTCAAGCCGGGAGAAACATTG	1020
QY	1258	GAATCCCTTGTTCANTGCTGGTTCAACCACTGGCAATGATGATTCTGACAAAGGAG	1317
Db	1021	GAATCCCTTGTTCACACANTGGTTTAAACCACTGATGATGATTCTGACAAAGGAA	1080
QY	1318	CAAGGTTAACCTTCCGTAATTTTACGGTATTACTACAGGTAATCAACACTCATGTGTTCT	1377
Db	1081	CAAGGTTATCTTCCGTAATTTTATGGGATTACTACAGGTAATCCCAACCAATGATGTTCCG	1140
QY	1378	TCGATGAATCTAAATTTGATTCACCTTCTCGAGGCAAGTCMAACGTAATGCTACGGAAC	1437
Db	1141	GCTATGAATCTAAATTTGATTCACCTTCTCTCGAGGCAAGTCMAACCTTTTGCTTATGTAACG	1200
QY	1438	CAACATGATTATTTTGAATCATCATGATATTTATCGGCTGAGACGAGAGAAAGGGACAAGCTCC	1497
Db	1201	CAGATGATTATCTTGAATCATCATGATATTTATCGGTTGAGACMAAGAGGGGAAATAGCTCC	1260
QY	1498	CACCCAAATTCAGGACTTGCACATCTATTATGTCGATGAGGCGCAGGGGGGTAATPAAATGATG	1557
Db	1261	CATCCAAATTCAGGACTTGCACATCTATTATGTCGATGATGTCGATGAGGCGGTAACMAATGATG	1320
QY	1558	TATGTCCGGAAAAATAAAGCTGCGCAAGTATGAGAGATATCACCGGAAATATAGTCTGGT	1617
Db	1321	TATGTCCGGAAAAATAAAGCGGGGCAAGTATGAGAGATATTTACCGGAAATATGAGACAGGC	1380
QY	1618	ACCGTCAACATTATATGATGATGTTGGGGGAAATTCACCTGTMAACGAGGGGCGAGTTTCG	1677
Db	1381	ACCGTCAACATTATATGATGATGAGATGAGGAGTATTTCTCTGTATATGAGAGGGGTCGTTTCG	1440
QY	1678	GTTTGGGTGAAGCAA	1692
Db	1441	GTTTGGGTGAAGCAA	1455

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RESULT 9
US-09-170-670-9
Sequence 9, Application US/09170670
Patent No. 6187576
GENERAL INFORMATION:
APPLICANT: Svendsen, Allan
APPLICANT: Borchert, Torben
APPLICANT: Bisgaard-Brantzen Henrik
TITLE OF INVENTION: Alpha-Amylase Mutants
FILE REFERENCE: 52/6,200-US
CURRENT APPLICATION NUMBER: US/09/170,670
CURRENT FILING DATE: 1998-10-13
EARLIER APPLICATION NUMBER: 1172/97
EARLIER FILING DATE: 1997-10-13
EARLIER APPLICATION NUMBER: 60/063,306
EARLIER FILING DATE: 1997-10-28
NUMBER OF SEQ ID NOS: 22
SOFTWARE: FastSeq for Windows Version 3.0.0
SEQ ID NO 9
LENGTH: 1455
TYPE: DNA
ORGANISM: Bacillus sp.

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US-09-170-670-9

Query Match 65.7%; Score 1167; DB 3; Length 1455;
Best Local Similarity 87.6%; Pred. No. 0;
Matches 1275; Conservative 0; Mismatches 180; Indels 0; Gaps 0;

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QY 238 CATCATATATGGAAGAAATGGGACCATGATGAGTATTTGATGATGCAATTTGCCAAATGAC 297
DB 1 CATCATATATGGAAGAAATGGTACTATGATGATGCAATTTGCCAAATGATTTGGCCAAATGAC 60
QY 298 GGGAAACCATGGAACAGGTGACGATGACGAGCTTAACCTTAAGATTAAGGATTAAC 357
DB 61 GGGAAATCATTTGGAACAGGTGAGGAGATGACGAGCTTAACCTTAAGATTAAGGATTAAC 120
QY 358 GCTGTTGATTCCTCTCTGATGGAAGGGGACTTCGCAAAATGATGTTGGGATGTC 417
DB 121 GCTGATGATTCCTCACTGATGGAAGGGGACTTCGCAAAATGATGATGATGAGCC 180
QY 418 TATGATTTGATGATCTTTGATGATTTAACCAAAAGGAAACGTCGTAACAAATATGAC 477
DB 181 TATGATTTATATATCTTTGATGATTTAACCAAAAGGAGCGGTTGATCAAAATATGGA 240
QY 478 ACAAGAGTATGATGGAAGGTCGATGACATCTTTGAAAATTAACGGGATTCAGTTTAT 537
DB 241 ACAAGCAACGATGACGCTGCGGTGACCTCTTTAAAAATTAACGGCATTCAGTATAT 300
QY 538 GGGGATGTCGATGATTAATCAATAAGGTGAGCAGACGGAACAGATGTTAAATGCGGTG 597
DB 301 GGTGATGTCGATGATTAATCAATAAGGTGAGCAGATGATGATGATGATGATGATGATG 360
QY 598 GAAATGATGGAAGCAACCAACCAAAATTAACGATGATTAACCAATGGAAGCATG 657
DB 361 GAAATGATGGAAGCAACCAACCAAAATTAACGATGATGATGATGATGATGATGATGATG 420
QY 658 ACGAAATTTGATTTCCCTGGAAGGAAATACCAATTCCTTAATGAGCGTGTAT 717
DB 421 ACGAAATTTGATTTCCCTGGAAGGAAATACCAATTCCTTAATGAGCGTGTAT 480
QY 718 CATTTGATGGAAGCAATTTGGATGATGATGATGATGATGATGATGATGATGATGATG 777
DB 481 CATTTGATGGAAGCAATTTGGATGATGATGATGATGATGATGATGATGATGATGATG 540
QY 778 AGAGATGCGGAAGGATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATG 837
DB 541 AGGGAACAGGCAAGGCTGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATG 600
QY 838 CTTATGATGGAAGCAATTTGGATGATGATGATGATGATGATGATGATGATGATGATG 897
DB 601 CTTATGATGGAAGCAATTTGGATGATGATGATGATGATGATGATGATGATGATGATG 660
QY 898 GGAATTTGATGGAAGCAATTTGGATGATGATGATGATGATGATGATGATGATGATG 957
DB 661 GGAATTTGATGGAAGCAATTTGGATGATGATGATGATGATGATGATGATGATGATG 720
QY 958 ATTAAATGACCTTAAGGATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGA 1017
DB 721 ATTAAATGACCTTAAGGATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGA 780
QY 1018 ATGTTTGAAGTGAAGCAATTTGGATGGAATGGAATGGAATGGAATGGAATGGAATG 1077
DB 781 ATGTTTGAAGTGAAGCAATTTGGATGGAATGGAATGGAATGGAATGGAATGGAATG 840
QY 1078 AAAACAGTTGGAATGATCTCGGTGATGATGATGATGATGATGATGATGATGATGATG 1137
DB 841 AAAACAGTTGGAATGATCTCGGTGATGATGATGATGATGATGATGATGATGATGATG 900
QY 1138 TCTATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1197
DB 901 TCTATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 960
QY 1198 CACCTATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1257
DB 961 CATCAACAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1020
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QY 1258 GAATCTTTGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1317
DB 1021 GAATCTTTGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1080
QY 1318 CAAGTTACCTTCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1377
DB 1081 CAAGTTACCTTCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1140
QY 1378 TCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1437
DB 1141 GCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1200
QY 1438 CAACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1497
DB 1201 CAGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1260
QY 1498 CACCAATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1557
DB 1261 CATCAATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1320
QY 1558 TATGTCGGAACATTAAGTGGCCAGATGATGATGATGATGATGATGATGATGATGATG 1617
DB 1321 TATGTCGGAACATTAAGTGGCCAGATGATGATGATGATGATGATGATGATGATGATG 1380
QY 1618 ACCGTACATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1677
DB 1381 ACCGTACATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1440
QY 1678 GTTGGTGAAGCA 1692
DB 1441 GTTGGTGAAGCA 1455
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RESULT 10
US-09-170-670-14
; Sequence 14, Application US/09170670
; Patent No. 6187576
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Borchert, Torben
; APPLICANT: Biegaard-Frantzen Henrik
; TITLE OF INVENTION: Alpha-Amylase Mutants
; FILE REFERENCE: 5276-200-US
; CURRENT APPLICATION NUMBER: US/09/170,670
; CURRENT FILING DATE: 1998-10-13
; EARLIER APPLICATION NUMBER: 1172/97
; EARLIER FILING DATE: 1997-10-13
; EARLIER APPLICATION NUMBER: 60/063,306
; EARLIER FILING DATE: 1997-10-28
; NUMBER OF SEQ. ID NOS: 22
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 14
; LENGTH: 1455
; TYPE: DNA
; ORGANISM: Bacillus sp.
US-09-170-670-14
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Query Match 65.7%; Score 1167; DB 3; Length 1455;
Best Local Similarity 87.6%; Pred. No. 0;
Matches 1275; Conservative 0; Mismatches 180; Indels 0; Gaps 0;

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QY 238 CATCATATATGGAAGAAATGGGACCATGATGAGTATTTGATGATGCAATTTGCCAAATGAC 297
DB 1 CATCATATATGGAAGAAATGGTACTATGATGATGCAATTTGCCAAATGATTTGGCCAAATGAC 60
QY 298 GGGAAACCATGGAACAGGTGACGATGACGAGCTTAACCTTAAGATTAAGGATTAAC 357
DB 61 GGGAAATCATTTGGAACAGGTGAGGAGATGACGAGCTTAACCTTAAGATTAAGGATTAAC 120
QY 358 GCTGTTGATTCCTCTCTGATGGAAGGGGACTTCGCAAAATGATGTTGGGATGTC 417
DB 121 GCTGATGATTCCTCACTGATGGAAGGGGACTTCGCAAAATGATGATGATGATGAGCC 180
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QY 418 TATGATTTGTCGATCTTGTGAGTTTAAACGAAAGGAAACCGCTGTAACAATATATGAC 477
DB 181 TATGATTTATATGATCTTGTGAGTTTAAACGAAAGGAAACCGCTGTAACAATATATGAC 240
QY 478 ACAAGAGTCAGTTGCAAGAGTCCGCTGACATCTTTGAAATAATACGGGATTCAGATTAT 537
DB 241 ACAGCAACACGACTACAGGCTGCGGTGACCTTTAAATAATACGGGATTCAGATTAT 300
QY 538 GGGGATGTCGTGATGATCATTAAGGTGAGCAGACGGGACAGAGATGTAATCCGCTG 597
DB 301 GGTATGTGTCATGAAATCATTAAGGTGAGCAGATGTAATGTAATGTAATCCGCTG 360
QY 598 GAAGTGAACCGAAGCAACGAAACCAAGAAATATAGGTGAATACCACTTGAACATG 657
DB 361 GAAGTGAATCGAGACACCGAAACCAAGAAACCTCAGAGAGTATGAAATGAAACCGCTG 420
QY 658 ACGAAATTTGATTTCCCTGGAAGAGAAATACCATTTCAACTTTAAATGGCGCTGAT 717
DB 421 ACAAGATTTGATTTCCCTGGAAGAGAAATACCATTTCAACTTTAAATGGCGCTGAT 480
QY 718 CATTTTGTGAGACATTTGGGATGATCAGTCAGCTTCAAGACAAATATATATATTC 777
DB 481 CATTTTGTGAGACATTTGGGATGATCAGTCAGCTTCAAAACAAATATATATATTC 540
QY 778 AGAGGTACCGGAAAGGACATGGGACCTGGGACATGATATAGGAACGGGACATATGATAC 837
DB 541 AGGGAAACGACAGGCTCGGACCTGGGACCTGGGACATGATATAGGAACGGGACATATG 600
QY 838 CTATATGATGACGACATTTGATGATGATCAGACAGATATCAATGAACTTAAATG 897
DB 601 CTATATGATGACGACATTTGATGATGATCAGACAGATATCAATGAACTTAAATG 660
QY 898 GGAATTTGATATCAATATCACTTATATGATGATTTAGATGATGATGATGATGAT 957
DB 661 GGAATTTGATATCAATATCACTTATATGATGATTTAGATGATGATGATGATGAT 720
QY 958 ATTAATATACGATATGACAGAGATTTGGCTAACACATGCGCTAACACACAGTAAACA 1017
DB 721 ATTAATATATACGATATGACAGAGATTTGGCTAACACATGCGCTAACACACAGTAAACA 780
QY 1018 ATGTTTGTGAGTGAATTTTGGAAATAATGACCTTGTGCAATGAAACCTATTTAAT 1077
DB 781 ATGTTTGTGAGTGAATTTTGGAAATAATGACCTTGTGCAATGAAACCTATTTAAT 840
QY 1078 AAAACAAAGTTGGAATCTCGCTGCTGCTGCTTCAATATATATTTGTACATGCA 1137
DB 841 AAAACAAAGTTGGAATCTCGCTGCTGCTGCTTCAATATATTTGTACATGCA 900
QY 1138 TCTATATAGTGGCTATTTTGTATGATGAAATATTTTAAATGCTTGTGTGACAAAA 1197
DB 901 TCTATATAGTGGCTATTTTGTATGATGAAATATTTTAAATGCTTGTGTGACAAAA 960
QY 1198 CACCTATACATGACATGATTTGTATACATGACCTGACGACGAGAGACATG 1257
DB 961 CATCAACACATGACCTGATTTGTGTATACATGATTTCTCAGCCCGGAGACATG 1020
QY 1258 GAATCTTTTGTCAATCGTGTCAAAACCACTGGCATATGATTTCTGACAAAGGAG 1317
DB 1021 GAATCTTTTGTCAATCGTGTCAAAACCACTGGCATATGATTTCTGACAAAGGAG 1080
QY 1318 CAAGTTATCCCTTCCGATTTTAAAGGTATATCAACGATACGATGCTTCT 1377
DB 1081 CAAGTTATCCCTTCCGATTTTAAAGGTATATCAACGATACGATGCTTCT 1140
QY 1378 TCGATGAATCTAAATATGATCACTTGTGACGACGTCAAACGATGCTTGTGACGAC 1437
DB 1441 GCTATGAATCTAAATATGATCACTTGTGACGACGTCAAACGATGCTTGTGACGAC 1200
QY 1438 CAACATGATTTATTTGATCATATGATATTTATCGGCTGACGAGAGAGGAGACGCTCC 1497
DB 1201 CAGATGATTTATTTGATCATATGATATTTATCGGCTGACGAGAGAGGAGAAATGCTCC 1260
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QY 1498 CACCAATTCAGAGCTTGCACTATTTATGTCGATGGGCGAGGGGATTAATATGATG 1557
DB 1261 CATCAATTCAGAGCTTGCACTATTTATGTCGATGGGCGAGGGGATTAATATGATG 1320
QY 1558 TATGTGGGAAACATTAAGCTGGCCCAATATGAGAGATATCACCGAAATAGTCTG 1617
DB 1321 TATGTGGGAAACATTAAGCTGGCCCAATATGAGAGATATTAACCGAAATAGGACAG 1380
QY 1618 ACCGTACCATTTATGACGATGTTGGGGAAATTTCACTGTAAACGGAGGGGAGTTG 1677
DB 1381 ACCGTACCATTTATGACGATGTTGGGGAAATTTCTGTAAATGAGAGGGTCCGTTG 1440
QY 1678 GTTGGGTGAGCA 1692
DB 1441 GTTGGGTGAGCA 1455

RESULT 11
US-09-193-068-9
; Sequence 9, Application US/09193068
; Patent No. 6197565
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Kjruiff, S ren
; APPLICANT: Bisgaard-Frantzen, Henrik
; APPLICANT: Andersen, Carsten
; TITLE OF INVENTION: Amylase Variants
; FILE REFERENCE: 5709.000-US
; CURRENT APPLICATION NUMBER: US/09/193.068
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 9
; LENGTH: 1455
; TYPE: DNA
; ORGANISM: Bacillus sp.
US-09-193-068-9

Query Match 65.7%; Score 1167; DB 3; Length 1455;
Best Local Similarity 87.6%; Pred. No. 0;
Matches 1275; Conservative 0; Mismatches 180; Indels 0; Gaps 0;

QY 238 CATCATATATGGAGAGATGGGACCATGATGACATTTTGAATGGCATTTGCCAAATGAC 297
DB 1 CATCATATATGGAGAGATGGGACCATGATGATGATGATGATGATGATGATGATGATGATG 60
QY 298 GGAACCACTGGAACAGGTTACGAGATGACGACGATTAATTAAGATTAAGGATTAAC 357
DB 61 GGAACCACTGGAACAGGTTACGAGATGACGACGATTAATTAAGATTAAGGATTAAC 120
QY 358 GCTGTTGATTTCTCTCTGACATGAGAGGACCTTGCAAAATGATGTTGGTATGCTCC 417
DB 121 GCTGTTGATTTCTCTCTGACATGAGAGGACCTTGCAAAATGATGTTGGTATGAGACCC 180
QY 418 TATGATTTGTCGATCTTGTGAGTTTAAACGAAAGGAAACCGCTGTAACAATATGAC 477
DB 181 TATGATTTATATGATCTTGTGAGTTTAAACGAAAGGAAACCGCTGTAACAATATGAC 240
QY 478 ACAAGAGTCAGTTGCAAGAGTCCGCTGACATCTTTGAAATAATACGGGATTCAGATTAT 537
DB 241 ACAGCAACACGACTACAGGCTGCGGTGACCTTTAAATAATACGGGATTCAGATTAT 300
QY 538 GGGGATGTCGTGATGATCATTAAGGTGAGCAGACGGGACAGAGATGTAATCCGCTG 597
DB 301 GGTATGTGTCATGAAATCATTAAGGTGAGCAGATGTAATGTAATGTAATCCGCTG 360
QY 598 GAAGTGAACCGAAGCAACGAAACCAAGAAATATAGGTGAATACCACTTGAACATG 657
DB 361 GAAGTGAATCGAGACACCGAAACCAAGAAACCTCAGAGAGTATGAAATGAAACCGCTG 420
QY 658 ACGAAATTTGATTTCCCTGGAAGAGAAATACCATTTCAACTTTAAATGGCGCTGAT 717
DB 421 ACAAGATTTGATTTCCCTGGAAGAGAAATACCATTTCAACTTTAAATGGCGCTGAT 480
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QY 718 CATTGATGGGACAGATTGGGATCGCTCAGCTCAGCTTGCAGAGCAAAATATATTAATTC 777
DB 481 CATTGATGGGACAGATTGGGATCGCTCAGCTCAGCTTGCAGAGCAAAATATATTAATTC 540
QY 778 AGAGGTACCGGAAAGGATGGGATCGGAGATAGATATAGAGACGGCACTATGATTAAC 837
DB 541 AGGGGAACGAGGACGGCTGGGATCGGAGATAGATATAGAGATAGGCACTATGATTAAC 600
QY 838 CTTATGATGACAGACATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 897
DB 601 CTTATGATGACAGACATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 660
QY 898 GGAGTTGGTATCAAAATACCTTAATCTGATGATGATGATGATGATGATGATGATGATGAT 957
DB 661 GGAGTTGGTATCAAAATACCTTAATCTGATGATGATGATGATGATGATGATGATGATGAT 720
QY 958 ATTAAATACAGCTATACGAGAGATGGCTAACACATGCTGCTAACACACAGGTAAACCA 1017
DB 721 ATTAAATACAGCTATACGAGAGATGGCTAACACATGCTGCTAACACACAGGTAAACCA 780
QY 1018 ATGTTGCACTGACAGATTTTGGAAAAATGACCTTGTGCAATCGAAAACTATTTAAT 1077
DB 781 ATGTTGCACTGACAGATTTTGGAAAAATGACCTTGTGCAATCGAAAACTATTTAAT 840
QY 1078 AAAACAAGTTGGAATCACTCGGTTGCGATGTTCTCTTCAATATATATTTGTCATGCA 1137
DB 841 AAAACAAGTTGGAATCACTCGGTTGCGATGTTCTCTTCAATATATATTTGTCATGCA 900
QY 1138 TCTAATAGTGGTGGCTATTTTGAATGAGAAATATTTAAATGTTCTGCTGTAACAAA 1197
DB 901 TCTAATAGTGGTGGCTATTTTGAATGAGAAATATTTAAATGTTCTGCTGTAACAAA 960
QY 1198 CACCTTATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1257
DB 961 CACCTTATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1020
QY 1258 GAATCTTTGTTCAATGCTGTTCAAAACACTGGCAATGATGATGATGATGATGATGATGAT 1317
DB 1021 GAATCTTTGTTCAATGCTGTTCAAAACACTGGCAATGATGATGATGATGATGATGATGAT 1080
QY 1318 CAAAGTTACCGTTCCGTAATTTTACCGTATGATGATGATGATGATGATGATGATGAT 1377
DB 1081 CAAAGTTACCGTTCCGTAATTTTACCGTATGATGATGATGATGATGATGATGATGAT 1140
QY 1378 TCGATGAAATCTAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1437
DB 1141 GCTATGAAATCTAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1200
QY 1438 CAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1497
DB 1201 CAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1260
QY 1498 CACCAATTCAGAGCTTGGCACTTATGATGATGATGATGATGATGATGATGATGATGAT 1557
DB 1261 CACCAATTCAGAGCTTGGCACTTATGATGATGATGATGATGATGATGATGATGATGAT 1320
QY 1558 TATGTTGGGAAAAATAGTGGCCAAATGATGATGATGATGATGATGATGATGATGATGAT 1617
DB 1321 TATGTTGGGAAAAATAGTGGCCAAATGATGATGATGATGATGATGATGATGATGATGAT 1380
QY 1618 ACCGTACCACTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1677
DB 1381 ACCGTACCACTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1440
QY 1678 GTTTGGGTGAAGCAA 1692
DB 1441 GTTTGGGTGAAGCAA 1455

RESULT 12
US-09-193-068-13
; Sequence 13, Application US/09193068

Patent No. 6197565
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Kjullif, S ren
; APPLICANT: Bisgaard-Frantzen, Henrik
; APPLICANT: Andersen, Carsten
; TITLE OF INVENTION: -Amylase Variants
; FILE REFERENCE: 5709,000-US
; CURRENT APPLICATION NUMBER: US/09/193,068
; CURRENT FILING DATE: 1998-11-16
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 13
; LENGTH: 1455
; TYPE: DNA
; ORGANISM: Bacillus sp.
; US-09-193-068-13

Query Match 65.7%; Score 1167; DB 3; Length 1455;
Best Local Similarity 87.6%; Pred. No. 0;
Matches 1275; Conservative 0; Mismatches 180; Indels 0; Gaps 0;

QY 238 CATCATTAATGGAAGCAATGGGACCATGATGACGATTTTGAATGCAATTTGCCAATGAC 297
DB 1 CATCATTAATGGAAGCAATGGGACCATGATGACGATTTTGAATGCAATTTGCCAATGAC 60
QY 298 GGGAAACCTGGAAAGGTTACGAGATGACGCGCTAATTAAGATTAAGGATTAAC 357
DB 61 GGGAAACCTGGAAAGGTTACGAGATGACGCGCTAATTAAGATTAAGGATTAAGGATTAAC 120
QY 358 GCTGTTGATTCCTCTCATAGGAAGGAGCTTCCGCAAAATGATGTTGGTATGCTGCC 417
DB 121 GCTGTTGATTCCTCTCATAGGAAGGAGCTTCCGCAAAATGATGTTGGTATGCTGCC 180
QY 418 TATGATTTGATGATCTTGGTATGATTAACCAAAAGGAAACGCTCCGTAACAAATATGTC 477
DB 181 TATGATTTGATGATCTTGGTATGATTAACCAAAAGGAAACGCTCCGTAACAAATATGTC 240
QY 478 ACAAGAGTCAAGTGAAGGATGCGGATGACATCTTTGAAAAATTAAGGGAATTCAGTTAT 537
DB 241 ACAAGAGTCAAGTGAAGGATGCGGATGACATCTTTGAAAAATTAAGGGAATTCAGTTAT 300
QY 538 GGGGATGCTGATGATGATGATTAAGGATGAGCAGGACAGAGATGATAATGCGGTG 597
DB 301 GGGGATGCTGATGATGATGATTAAGGATGAGCAGAGATGATAATGATAATGCGGTG 360
QY 598 GAAATGAAACCGAAAGCAACGAAACCAAGAAATATCGTGAATACCATGTAAGCATG 657
DB 361 GAAATGAAACCGAAAGCAACGAAACCAAGAAATATCGTGAATACCATGTAAGCATG 420
QY 658 ACGAATTTGATTTCCCTGGAAGAGGAATTAACCATTCACATTTAAATGGGCTGAT 717
DB 421 ACGAATTTGATTTCCCTGGAAGAGGAATTAACCATTCACATTTAAATGGGCTGAT 480
QY 718 CATTTTGATGGGACAGATTTGGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 777
DB 481 CATTTTGATGGGACAGATTTGGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 540
QY 778 AGAGGTACCGGAAAGGATGGGATCGGAGATAGATATAGAGACGGCACTATGATTAAC 837
DB 541 AGGGGAACGAGGACGGCTGGGATCGGAGATAGATATAGAGATAGGCACTATGATTAAC 600
QY 838 CTTATGATGACAGACATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 897
DB 601 CTTATGATGACAGACATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 660
QY 898 GGAGTTGGTATCAAAATACCTTAATCTGATGATGATGATGATGATGATGATGATGATGAT 957
DB 661 GGAGTTGGTATCAAAATACCTTAATCTGATGATGATGATGATGATGATGATGATGATGAT 720
QY 958 ATTAAATACAGCTATACGAGAGATGGCTAACACATGCTGCTAACACACAGGTAAACCA 1017
DB 721 ATTAAATACAGCTATACGAGAGATGGCTAACACATGCTGCTAACACACAGGTAAACCA 780

QY 1018 ATGTTGAGTTGAGAAATTTGGAAAATGACCTTGCTGAGCAAGAAACATTTAAT 1077
 DB 781 ATGTTGAGTTGAGAAATTTGGAAAATGACCTTGCTGAGCAAGAAACATTTAAT 840
 QY 1078 AAAACAAGTTGGAATCACTCCGTTGTCAGATGTTCTCTTCAATTAATTTGACAAATCA 1137
 DB 841 AAAACAAGTTGGAATCACTCCGTTGTCAGATGTTCTCTTCAATTAATTTGACAAATCA 900
 QY 1138 TCTAATAGTGGTGTATTTGATATGCAAAATATTTAAATGTTCTGTGTCGTAACAAA 1197
 DB 901 TCTAATAGTGGTGTATTTGATATGCAAAATATTTAAATGTTCTGTGTCGTAACAAA 960
 QY 1198 CACCTTATACATGAGTACATTTGTTGATACCACTGCTCAGCCGAGGAAAGCATG 1257
 DB 961 CATCAACACATGCGCTTACTTGTGTATTAACATGATTCAGCCCGGAGGAAAGCATG 1020
 QY 1258 GAATCTTTGTTCAATCGTGTTCAAACCACTGAGCATATGATTTCTGACAAAGGAG 1317
 DB 1021 GAATCTTTGTTCAATCGTGTTCAAACCACTGAGCATATGATTTCTGACAAAGGAG 1080
 QY 1318 CAAGTTACCTTCCTGATTTTAAAGGTGATTAAGTATTAACCACTGATGTTCT 1377
 DB 1081 CAAGTTACCTTCCTGATTTTAAAGGTGATTAAGTATTAACCACTGATGTTCT 1140
 QY 1378 TCGATGAAATCTAAATGATCACTTCTGAGGAGCATCAAGCATATGCTTACGAAAC 1437
 DB 1141 GCTATGAAATCTAAATGATCACTTCTGAGGAGCATCAAGCATATGCTTACGAAAC 1200
 QY 1438 CAACATGATTTATTTGATCATGATATTAATCGGCTGAGCAAGAGAGGAGACAGTCC 1497
 DB 1201 CAGATGATTTATTTGATCATGATATTAATCGGCTGAGCAAGAGAGGAGAAATAGCTCC 1260
 QY 1498 CACCAATTCAGACCTTGCAATTTATGTCGATGAGGAGGAGGATTAATTAATGATG 1557
 DB 1261 CATCAATTCAGACCTTGCAATTTATGTCGATGAGGAGGAGGATTAATTAATGATG 1320
 QY 1558 TATGCGGAGAAACATTAAGCTGAGCAAGTATGAGAGATATCACCGGAAATAGTCTGCT 1617
 DB 1321 TATGCGGAGAAACATTAAGCTGAGCAAGTATGAGAGATATTAATTAATTAATGAGAGG 1380
 QY 1618 ACCGTCAACATTAATGAGATGTTGGGAGATTTCACTGTAACGAGAGGAGGATTTG 1677
 DB 1381 ACCGTCAACATTAATGAGATGTTGGGAGATTTCTCTGTAATGAGAGGATTTGCTG 1440
 QY 1678 GTTGGGTGAAGCA 1692
 DB 1441 GTTGGGTGAAGCA 1455
 RESULT 13
 US-09-183-412-9
 ; Sequence 9, Application US/09183412
 ; Patent No. 6204232
 ; GENERAL INFORMATION:
 ; APPLICANT: Borchert, Torben V.
 ; APPLICANT: Svendsen, Allan
 ; APPLICANT: Andersen, Carsten
 ; APPLICANT: Nielsen, Bjarne
 ; APPLICANT: Nielsen, Torben L.
 ; APPLICANT: Kjaerulf, Soren
 ; TITLE OF INVENTION: Alpha-Amylase Mutants
 ; FILE REFERENCE: 5368.200-US
 ; CURRENT APPLICATION NUMBER: US/09/183,412
 ; CURRENT FILING DATE: 1998-10-30
 ; EARLIER APPLICATION NUMBER: 60/064,662
 ; EARLIER FILING DATE: 1997-11-06
 ; EARLIER APPLICATION NUMBER: 60/093,234
 ; EARLIER FILING DATE: 1998-07-17
 ; EARLIER APPLICATION NUMBER: 1240/97
 ; EARLIER FILING DATE: 1997-10-30
 ; EARLIER APPLICATION NUMBER: PA 1998 00936
 ; EARLIER FILING DATE: 1998-07-14

NUMBER OF SEQ ID NOS: 58
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO: 9
 ; LENGTH: 1455
 ; TYPE: DNA
 ; ORGANISM: Bacillus
 US-09-183-412-9
 Query Match 65.74; Score 1167; DB 3; Length 1455;
 Best Local Similarity 87.6%; Pred. No. 0;
 Matches 1275; Conservative 0; Mismatches 180; Indels 0; Gaps 0;
 QY 238 CATCATATGAGGAGAAATGAGGAGCATGATGATGATTTGTAATGAGCATTTGCCAAATGAC 297
 DB 1 CATCATATGAGGAGAAATGAGGAGCATGATGATGATTTGTAATGAGCATTTGCCAAATGAC 60
 QY 298 GGGAAACCACTGGAACAGGTTACGAGATGACCGACATTAATTTAAAGATTAAGGATTAAC 357
 DB 61 GGGAAATCATGGAACAGGTTAGGAGATGACCGACATTAATTTAAAGATTAAGGATTAAC 120
 QY 358 GCTGTTGATTTCTCTCTGATGAGAGGAGCTTCCGAAATGATTTGGTATGATGCC 417
 DB 121 GCTGATGATTTCTCTCTGATGAGAGGAGCTTCCGAAATGATTTGGTATGATGCC 180
 QY 418 TATGATTTGATGATTTGATGATTTTAAACCAAGGAGACCGTCCGTAACAAATATGAC 477
 DB 181 TATGATTTGATGATTTGATGATTTTAAACCAAGGAGACCGTCCGTAACAAATATGAC 240
 QY 478 ACAAGAGTCACTGGAACAGGTTACCGATGATCTTTGAAATTAACGAGATTAAGTAT 537
 DB 241 ACAAGAGTCACTGGAACAGGTTACCGATGATCTTTGAAATTAACGAGATTAAGTAT 300
 QY 538 GGGATGCTGATGATTAATTAAGTATGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 597
 DB 301 GGGATGCTGATGATTAATTAAGTATGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 360
 QY 598 GAGTGAACCGAGAACCGGAAACCAAGAAATATCAGGTGATTAACCATTAAGGAGGATG 657
 DB 361 GAGTGAACCGAGAACCGGAAACCAAGAAATATCAGGTGATTAACCATTAAGGAGGATG 420
 QY 658 ACGAAATTTGATTTCCCTGGAAGAGAAATACCATTTCAATTTAAATGAGCGGTGAT 717
 DB 421 ACGAAATTTGATTTCCCTGGAAGAGAAATACCATTTCAATTTAAATGAGCGGTGAT 480
 QY 718 CATTTGATGAGGAGATTTGGATCACTCAGTCACTTCAAGAACAAATATTAATTC 777
 DB 481 CATTTGATGAGGAGATTTGGATCACTCAGTCACTTCAAGAACAAATATTAATTC 540
 QY 778 AGAGTACCGGAAAGGAGATGAGGAGTGGAGATTAATGAGAGGAGGAGGAGGAGGAGGAG 837
 DB 541 AGAGTACCGGAAAGGAGATGAGGAGTGGAGATTAATGAGAGGAGGAGGAGGAGGAGGAG 600
 QY 838 CTATGATGAGGAGATTTGATGATGATCACTCAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 897
 DB 601 CTATGATGAGGAGATTTGATGATGATCACTCAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 660
 QY 898 GAGTGTGATTAACAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 957
 DB 661 GAGTGTGATTAACAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 720
 QY 958 ATTAAATACGCTTATGAGAGATTTGAGGAGTGGAGTAAACATGAGGAGTAAACAGGAGTAA 1017
 DB 721 ATTAAATACGCTTATGAGAGATTTGAGGAGTGGAGTAAACATGAGGAGTAAACAGGAGTAA 780
 QY 1018 ATGTTGAGTGGAGATTTTGGAAAATGACCTTCTGCAATCGAAATCTATTTAAT 1077
 DB 781 ATGTTGAGTGGAGATTTTGGAAAATGACCTTCTGCAATCGAAATCTATTTAAT 840
 QY 1078 AAAACAAGTTGGAATCACTCCGTTGTCAGATGTTCTCTTCAATTAATTTGACAAATCA 1137
 DB 841 AAAACAAGTTGGAATCACTCCGTTGTCAGATGTTCTCTTCAATTAATTTGACAAATCA 900
 QY 1138 TCTAATAGTGGTGTATTTGATATGCAAAATATTTAAATGTTCTGTGTCGTAACAAA 1197


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Db      ||||| 1198 1258 1318 1378 1438 1558 1618 1678 1738 1798 1858 1918 1978 2038 2098 2158 2218 2278 2338 2398 2458 2518 2578 2638 2698 2758 2818 2878 2938 2998 3058 3118 3178 3238 3298 3358 3418 3478 3538 3598 3658 3718 3778 3838 3898 3958 4018 4078 4138 4198 4258 4318 4378 4438 4498 4558 4618 4678 4738 4798 4858 4918 4978 5038 5098 5158 5218 5278 5338 5398 5458 5518 5578 5638 5698 5758 5818 5878 5938 5998 6058 6118 6178 6238 6298 6358 6418 6478 6538 6598 6658 6718 6778 6838 6898 6958 7018 7078 7138 7198 7258 7318 7378 7438 7498 7558 7618 7678 7738 7798 7858 7918 7978 8038 8098 8158 8218 8278 8338 8398 8458 8518 8578 8638 8698 8758 8818 8878 8938 8998 9058 9118 9178 9238 9298 9358 9418 9478 9538 9598 9658 9718 9778 9838 9898 9958 10018 10078 10138 10198 10258 10318 10378 10438 10498 10558 10618 10678 10738 10798 10858 10918 10978 11038 11098 11158 11218 11278 11338 11398 11458 11518 11578 11638 11698 11758 11818 11878 11938 11998 12058 12118 12178 12238 12298 12358 12418 12478 12538 12598 12658 12718 12778 12838 12898 12958 13018 13078 13138 13198 13258 13318 13378 13438 13498 13558 13618 13678 13738 13798 13858 13918 13978 14038 14098 14158 14218 14278 14338 14398 14458 14518 14578 14638 14698 14758 14818 14878 14938 14998 15058 15118 15178 15238 15298 15358 15418 15478 15538 15598 15658 15718 15778 15838 15898 15958 16018 16078 16138 16198 16258 16318 16378 16438 16498 16558 16618 16678 16738 16798 16858 16918 16978 17038 17098 17158 17218 17278 17338 17398 17458 17518 17578 17638 17698 17758 17818 17878 17938 17998 18058 18118 18178 18238 18298 18358 18418 18478 18538 18598 18658 18718 18778 18838 18898 18958 19018 19078 19138 19198 19258 19318 19378 19438 19498 19558 19618 19678 19738 19798 19858 19918 19978 20038 20098 20158 20218 20278 20338 20398 20458 20518 20578 20638 20698 20758 20818 20878 20938 20998 21058 21118 21178 21238 21298 21358 21418 21478 21538 21598 21658 21718 21778 21838 21898 21958 22018 22078 22138 22198 22258 22318 22378 22438 22498 22558 22618 22678 22738 22798 22858 22918 22978 23038 23098 23158 23218 23278 23338 23398 23458 23518 23578 23638 23698 23758 23818 23878 23938 23998 24058 24118 24178 24238 24298 24358 24418 24478 24538 24598 24658 24718 24778 24838 24898 24958 25018 25078 25138 25198 25258 25318 25378 25438 25498 25558 25618 25678 25738 25798 25858 25918 25978 26038 26098 26158 26218 26278 26338 26398 26458 26518 26578 26638 26698 26758 26818 26878 26938 26998 27058 27118 27178 27238 27298 27358 27418 27478 27538 27598 27658 27718 27778 27838 27898 27958 28018 28078 28138 28198 28258 28318 28378 28438 28498 28558 28618 28678 28738 28798 28858 28918 28978 29038 29098 29158 29218 29278 29338 29398 29458 29518 29578 29638 29698 29758 29818 29878 29938 29998 30058 30118 30178 30238 30298 30358 30418 30478 30538 30598 30658 30718 30778 30838 30898 30958 31018 31078 31138 31198 31258 31318 31378 31438 31498 31558 31618 31678 31738 31798 31858 31918 31978 32038 32098 32158 32218 32278 32338 32398 32458 32518 32578 32638 32698 32758 32818 32878 32938 32998 33058 33118 33178 33238 33298 33358 33418 33478 33538 33598 33658 33718 33778 33838 33898 33958 34018 34078 34138 34198 34258 34318 34378 34438 34498 34558 34618 34678 34738 34798 34858 34918 34978 35038 35098 35158 35218 35278 35338 35398 35458 35518 35578 35638 35698 35758 35818 35878 35938 35998 36058 36118 36178 36238 36298 36358 36418 36478 36538 36598 36658 36718 36778 36838 36898 36958 37018 37078 37138 37198 37258 37318 37378 37438 37498 37558 37618 37678 37738 37798 37858 37918 37978 38038 38098 38158 38218 38278 38338 38398 38458 38518 38578 38638 38698 38758 38818 38878 38938 38998 39058 39118 39178 39238 39298 39358 39418 39478 39538 39598 39658 39718 39778 39838 39898 39958 40018 40078 40138 40198 40258 40318 40378 40438 40498 40558 40618 40678 40738 40798 40858 40918 40978 41038 41098 41158 41218 41278 41338 41398 41458 41518 41578 41638 41698 41758 41818 41878 41938 41998 42058 42118 42178 42238 42298 42358 42418 42478 42538 42598 42658 42718 42778 42838 42898 42958 43018 43078 43138 43198 43258 43318 43378 43438 43498 43558 43618 43678 43738 43798 43858 43918 43978 44038 44098 44158 44218 44278 44338 44398 44458 44518 44578 44638 44698 44758 44818 44878 44938 44998 45058 45118 45178 45238 45298 45358 45418 45478 45538 45598 45658 45718 45778 45838 45898 45958 46018 46078 46138 46198 46258 46318 46378 46438 46498 46558 46618 46678 46738 46798 46858 46918 46978 47038 47098 47158 47218 47278 47338 47398 47458 47518 47578 47638 47698 47758 47818 47878 47938 47998 48058 48118 48178 48238 48298 48358 48418 48478 48538 48598 48658 48718 48778 48838 48898 48958 49018 49078 49138 49198 49258 49318 49378 49438 49498 49558 49618 49678 49738 49798 49858 49918 49978 50038 50098 50158 50218 50278 50338 50398 50458 50518 50578 50638 50698 50758 50818 50878 50938 50998 51058 51118 51178 51238 51298 51358 51418 51478 51538 51598 51658 51718 51778 51838 51898 51958 52018 52078 52138 52198 52258 52318 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RESULT 15

US-09-354-191A-4
 ; Sequence 4, Application US/09354191A
 ; Patent No. 6297038
 ; GENERAL INFORMATION:
 ; APPLICANT: Bisgaard-Frantzen, Henrik
 ; APPLICANT: Svendsen, Allan
 ; APPLICANT: Borchert, Torben Vedel
 ; TITLE OF INVENTION: AMYLASE VARIANTS
 ; NUMBER OF SEQUENCES: 32
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESS: No. 62970380 No. 6297038disk of No. 6297038th America, Inc.
 ; STREET: 405 Lexington Avenue, Suite 6400
 ; CITY: New York
 ; STATE: New York
 ; COUNTRY: U.S.A.
 ; ZIP: 10174-6401
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent in Release #1.0, Version #1.25 (EPO)
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/354,191A
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/600,656
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Lambiris, Elias J.
 ; REGISTRATION NUMBER: 33,728
 ; REFERENCE/DOCKET NUMBER: 4318, 204-US
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 212 867 0123
 ; TELEFAX: 212 867 0298
 ; INFORMATION FOR SEQ ID NO: 4:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1455 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: DNA (genomic)

US-09-354-191A-4

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GenCore version 5.1.6
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OM nucleic - nucleic search, using bw model

Run on: May 2, 2005, 19:03:32 ; Search time 725 Seconds
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Searched: 5642217 seqs, 3043843248 residues

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Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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13	1167	65.7	1455	14	US-10-025-648-4	Sequence 4, Appli
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ALIGNMENTS

RESULT 1
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; Sequence 1, Application US/09986676A
; Patent No. US20020102698A1
; GENERAL INFORMATION:
; APPLICANT: HATADA, Yuji
; APPLICANT: OZAKI, Katsuya
; APPLICANT: ARA, Katsutoshi
; APPLICANT: KAWAI, Shuji
; APPLICANT: ITO, Susumu
; TITLE OF INVENTION: Gene Encoding Alkaline Liquefying Alpha-Amylase
; FILE REFERENCE: 2173-0121P
; CURRENT APPLICATION NUMBER: US/09/986, 676A
; PRIOR FILING DATE: 2001-11-09
; PRIOR APPLICATION NUMBER: PCT/JP96/01641
; PRIOR FILING DATE: 1996-06-14
; PRIOR APPLICATION NUMBER: Japan 147257/1995
; PRIOR FILING DATE: 1995-06-14
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 1776
; TYPE: DNA
; ORGANISM: Bacillus sp.
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (145)..(1692)
; OTHER INFORMATION:
US-09-986-676A-1
Query Match 100.0%; Score 1776; DB 9; Length 1776;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1776; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 ATATAATTTGAATGAACCTTATGAAATATGATGGATGGCGGACGAGAAAAAC 60
DB 1 ATATAATTTGAATGAACCTTATGAAATATGATGGATGGCGGACGAGAAAAAC 60
QY 61 TTGGAGATTAGGAAGTATTAAGGATTTTTTTTGACTTGTGTGMAAACCTTGCA 120
DB 61 TTGGAGATTAGGAAGTATTAAGGATTTTTTTTGACTTGTGTGMAAACCTTGCA 120
QY 121 AAATGGAAGAGAGGGCTTTTATGAACTTCATACCGTATTAATAGCGTACTT 180
DB 121 AAATGGAAGAGAGGGCTTTTATGAACTTCATACCGTATTAATAGCGTACTT 180
QY 181 AACCTATGTTAGCTGATGCTGTTTGTTCATATGACGGAACGAGACAGCCAT 240
DB 181 AACCTATGTTAGCTGATGCTGTTTGTTCATATGACGGAACGAGACAGCCAT 240
QY 241 CATATATGGAAGGATGGGACCATGATGCAATTTTGAATGGAATTTGCCMAATG 300
DB 241 CATATATGGAAGGATGGGACCATGATGCAATTTTGAATGGAATTTGCCMAATG 300
QY 301 AACCACTGGAACAGTTTACGATGACGACGCTTACTTAAAGGTAAAGGATTCG 360
DB 301 AACCACTGGAACAGTTTACGATGACGACGCTTACTTAAAGGTAAAGGATTCG 360
QY 361 GTTTGATTCCTCTGATGGAAGGGGACTTGGCAAAATGATGTGGGTATGGCTAT 420
DB 361 GTTTGATTCCTCTGATGGAAGGGGACTTGGCAAAATGATGTGGGTATGGCTAT 420
QY 421 GATTTGATGATCTTGTGTGATTTAACCAAAAGGGAACCGTCCGTACAAATATG 480
DB 421 GATTTGATGATCTTGTGTGATTTAACCAAAAGGGAACCGTCCGTACAAATATG 480
QY 481 AGGAGTCAATGTCGAAGGTGCGGTCACATCTTTGAAAATAACGGGATTCAGTT 540
DB 481 AGGAGTCAATGTCGAAGGTGCGGTCACATCTTTGAAAATAACGGGATTCAGTT 540
QY 541 GATGTCGTGATGATCTATAAGGTGAGCAGACGGGACAGATGTAAATGCGGTGA 600
DB 541 GATGTCGTGATGATCTATAAGGTGAGCAGACGGGACAGATGTAAATGCGGTGA 600
QY 601 GTGACCGGAAGCAACCGAAACCAAGAAATATCAGGTGATATCACATTTGAAG 660
DB 601 GTGACCGGAAGCAACCGAAACCAAGAAATATCAGGTGATATCACATTTGAAG 660
QY 661 AAATTTGATTTCCCTGGAAGGAAATACCATTCGAATTTAAATGGCGTGTATCA 720
DB 661 AAATTTGATTTCCCTGGAAGGAAATACCATTCGAATTTAAATGGCGTGTATCA 720
QY 721 TTTGATGGGACAGATTTGGGATCAGTCACTGCTCAGACCTTCAAGAACAAATAT 780
DB 721 TTTGATGGGACAGATTTGGGATCAGTCACTGCTCAGACCTTCAAGAACAAATAT 780
QY 781 GGTATCCGGAAGGATGGGACTGGGAAGTATATAGAGACGGCACTATGATTACCT 840
DB 781 GGTATCCGGAAGGATGGGACTGGGAAGTATATAGAGACGGCACTATGATTACCT 840
QY 841 ATGATATCAAGCATTTGATATGATCATCCAGAGATTAATCAATGAACTTTAGAA 900
DB 841 ATGATATCAAGCATTTGATATGATCATCCAGAGATTAATCAATGAACTTTAGAA 900
QY 901 GTTTGATTCATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 960
DB 901 GTTTGATTCATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 960
QY 961 AAATACAGTATACGAGAGATTTGCTTAACATGTCGTAAACACACAGGTAAAC 1020
DB 961 AAATACAGTATACGAGAGATTTGCTTAACATGTCGTAAACACACAGGTAAAC 1020
QY 1021 TTTGCAAGTTCAGAAATTTTGGAAAAATGACCTTCTGCAATCGAAAACTATTT 1080
DB 1021 TTTGCAAGTTCAGAAATTTTGGAAAAATGACCTTCTGCAATCGAAAACTATTT 1080
QY 1081 ACAAGTTGAATCACTCGGTGTCGATGTTCCCTTCAATTAATTTGTACAATGATCT 1140

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DB 1081 ACAAGTTGAATCACTCGGTGTCGATGTTCCCTTCAATTAATTTGTACAATGATCT 1140
QY 1141 AATAGTGTGGCTATTTTGTATATGAGAAATTTTAAATGTTCTGTCTTAACAAAAC 1200
DB 1141 AATAGTGTGGCTATTTTGTATATGAGAAATTTTAAATGTTCTGTCTTAACAAAAC 1200
QY 1201 CCTATACATGCACTGATTTGTATGATTAACATGACTCTCAGCCAGAGAGAGATTG 1260
DB 1201 CCTATACATGCACTGATTTGTATGATTAACATGACTCTCAGCCAGAGAGATTG 1260
QY 1261 TCCTTTGTTCAATCGTGTGTTCAAAACCATGGAATATGATATTTCTGAACAAG 1320
DB 1261 TCCTTTGTTCAATCGTGTGTTCAAAACCATGGAATATGATATTTCTGAACAAG 1320
QY 1321 GGTATACCTTCGGTATTTTATAGGTATATCTAGAGATACCAATGATGTTCTT 1380
DB 1321 GGTATACCTTCGGTATTTTATAGGTATATCTAGAGATACCAATGATGTTCTT 1380
QY 1381 ATGAATCTTAAATTTGATCACTTCTGACAGGACGTCGAACGATGCTTACGGA 1440
DB 1381 ATGAATCTTAAATTTGATCACTTCTGACAGGACGTCGAACGATGCTTACGGA 1440
QY 1441 CATGATTAATTTGATCATATGATATATATCGCTGAGCAGAGAGAGAGAGAG 1500
DB 1441 CATGATTAATTTGATCATATGATATATATCGCTGAGCAGAGAGAGAGAGAG 1500
QY 1501 CCATATTCAGAGATTTGCACTATATATGTCGATGGGCGCAGGGGTAAATTA 1560
DB 1501 CCATATTCAGAGATTTGCACTATATATGTCGATGGGCGCAGGGGTAAATTA 1560
QY 1561 GTGCGGAACATTAACCTGCGCAAGTATGAGAGATATCACCGGAATGTTGTG 1620
DB 1561 GTGCGGAACATTAACCTGCGCAAGTATGAGAGATATCACCGGAATGTTGTG 1620
QY 1621 GTCCACATTAATGATGATGATGATGATGATGATGATGATGATGATGATG 1680
DB 1621 GTCCACATTAATGATGATGATGATGATGATGATGATGATGATGATGATG 1680
QY 1681 TGGGTGAGCAATTAATTAAGGAACAGAGCGCAAAATTTCTTCCATATGACAG 1740
DB 1681 TGGGTGAGCAATTAATTAAGGAACAGAGCGCAAAATTTCTTCCATATGACAG 1740
QY 1741 CCGATCACTATACCCCAATATTAATTTGAAAGCTT 1776
DB 1741 CCGATCACTATACCCCAATATTAATTTGAAAGCTT 1776

RESULT 2
US-10-399-161-7
; Sequence 7, Application US/10399161
; Publication No. US20040091994A1
; GENERAL INFORMATION:
; APPLICANT: Andersen, Carsten
; TITLE OF INVENTION: Alpha-amylase variant with altered properties
; FILE REFERENCE: 10115.204-WO
; CURRENT APPLICATION NUMBER: US/10/399,161
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 7
; LENGTH: 1776
; TYPE: DNA
; ORGANISM: Bacillus sp.
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (145)..(1692)
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: (145)..(238)
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: (238)..()

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US-10-399-161-7

Query Match 100.0%; Score 1776; DB 17; Length 1776;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1776; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 ATATATAATTTGAAATGACACCTATGAAATATGAGCATTTGGCCGACGAGAAAAAC 60
 1 ATATATAATTTGAAATGACACCTATGAAATATGAGCATTTGGCCGACGAGAAAAAC 60
 61 TTGGAGTTAGGAGATGATTAATTAAGATTTTGTGACTGTGTGAAAACGCTTCAT 120
 61 TTGGAGTTAGGAGATGATTAATTAAGATTTTGTGACTGTGTGAAAACGCTTCAT 120
 121 AAATGAAGAGAGGGGTCTTTTATGAAACCTTCAATCCGTAATTAATTAAGTACTATTA 180
 121 AAATGAAGAGAGGGGTCTTTTATGAAACCTTCAATCCGTAATTAATTAAGTACTATTA 180
 121 AAATGAAGAGAGGGGTCTTTTATGAAACCTTCAATCCGTAATTAATTAAGTACTATTA 180
 181 ACACTATTGTTAGCTGTAGCTGTTTGTTCATATATGACGGAACGACAGCCCAT 240
 181 ACACTATTGTTAGCTGTAGCTGTTTGTTCATATATGACGGAACGACAGCCCAT 240
 241 CATAATGAGAGCAATGAGGACCATGATGCAATTTTGAATGGCAATTTGCCAATGACGG 300
 241 CATAATGAGAGCAATGAGGACCATGATGCAATTTTGAATGGCAATTTGCCAATGACGG 300
 301 AACCACTGGAACAGTTACGAGATGACGAGCTTAATTAAGATTAAGGATTAACCGCT 360
 301 AACCACTGGAACAGTTACGAGATGACGAGCTTAATTAAGATTAAGGATTAACCGCT 360
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 361 GTTTGGATTCTCTGCAATGAGAGGACCTTGCAGAAATGATGTTGGGATGCTCAT 420
 361 GTTTGGATTCTCTGCAATGAGAGGACCTTGCAGAAATGATGTTGGGATGCTCAT 420
 421 GATTTGATGATCTTGTGATGTTTAAACCAAAAGGAAACCGTCCGTAACAAATATGACA 480
 421 GATTTGATGATCTTGTGATGTTTAAACCAAAAGGAAACCGTCCGTAACAAATATGACA 480
 481 AGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 540
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 481 AGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 540
 541 GATGTCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 600
 541 GATGTCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 600
 601 GTGAAACGAGAGCAACCAAGAAATATCAGGTGATATACACCATTTGAAGCATGACG 660
 601 GTGAAACGAGAGCAACCAAGAAATATCAGGTGATATACACCATTTGAAGCATGACG 660
 601 GTGAAACGAGAGCAACCAAGAAATATCAGGTGATATACACCATTTGAAGCATGACG 660
 661 AAATTTGATTTTCTCGAAGAGAAATACCATTTCAACTTTAAATGGCGCTGTATCAT 720
 661 AAATTTGATTTTCTCGAAGAGAAATACCATTTCAACTTTAAATGGCGCTGTATCAT 720
 721 TTGATGAGAGAGATTTGGGATGATGATGATGATGATGATGATGATGATGATGATGAT 780
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 781 GTGACCGGAAAGGATGAGGATGAGGATGATGATGATGATGATGATGATGATGATGAT 840
 781 GTGACCGGAAAGGATGAGGATGAGGATGATGATGATGATGATGATGATGATGATGAT 840
 841 ATGATGAGAGATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 900
 841 ATGATGAGAGATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 900
 901 GTTTGGTATTAACCAATATGATTAATTAAGTATTAAGTATTAAGTATTAAGTATTAAG 960
 901 GTTTGGTATTAACCAATATGATTAATTAAGTATTAAGTATTAAGTATTAAGTATTAAG 960
 961 AAATACAGCTATACAGAGATTTGGCTTAACATGTCGTTAACACCAAGGATTAACCAT 1020
 961 AAATACAGCTATACAGAGATTTGGCTTAACATGTCGTTAACACCAAGGATTAACCAT 1020

1021 TTGCAAGTTGAGATTTTGGAAAAATGACCTGTGCAATGCAAACTATTTAATAA 1080
 1021 TTGCAAGTTGAGATTTTGGAAAAATGACCTGTGCAATGCAAACTATTTAATAA 1080
 1081 ACAAGTTGAAATCACTCCGTGTGATGATGATGATGATGATGATGATGATGATGAT 1140
 1081 ACAAGTTGAAATCACTCCGTGTGATGATGATGATGATGATGATGATGATGATGAT 1140
 1141 AATAGTGTGCTATTTTGAATGAGAAATTTTAAATGTTCTGTGTAACAAACAC 1200
 1141 AATAGTGTGCTATTTTGAATGAGAAATTTTAAATGTTCTGTGTAACAAACAC 1200
 1201 CCTATACATGACATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1260
 1201 CCTATACATGACATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1260
 1261 TCCTTTGTTCAATCGTGTGCAAAACCACTGCAATGATGATGATGATGATGATGAT 1320
 1261 TCCTTTGTTCAATCGTGTGCAAAACCACTGCAATGATGATGATGATGATGATGAT 1320
 1321 GGTACCTTCGTAATTTTACGATGATGATGATGATGATGATGATGATGATGATGAT 1380
 1321 GGTACCTTCGTAATTTTACGATGATGATGATGATGATGATGATGATGATGATGAT 1380
 1381 ATGAAATGTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1440
 1381 ATGAAATGTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1440
 1441 CATGATTTATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1500
 1441 CATGATTTATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1500
 1501 CCAATTTGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1560
 1501 CCAATTTGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1560
 1561 GTGCGGAAACATTAAGCTGCGCAAGATGAGAGATGATGATGATGATGATGATGAT 1620
 1561 GTGCGGAAACATTAAGCTGCGCAAGATGAGAGATGATGATGATGATGATGATGAT 1620
 1621 GTACACATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1680
 1621 GTACACATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1680
 1681 TGGGTGAAGCAATTAATTAAGGACAGAGGCAAAATTAATTAATTAATTAATTAAT 1740
 1681 TGGGTGAAGCAATTAATTAAGGACAGAGGCAAAATTAATTAATTAATTAATTAAT 1740
 1741 CCGATCACTCATACCAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1776
 1741 CCGATCACTCATACCAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1776

RESULT 3
 US-09-971-611-1
 ; Sequence 1, Application US/09971611
 ; Patent No. US20020123124A1
 ; GENERAL INFORMATION:
 ; APPLICANT: ENDO, KEIJI
 ; APPLICANT: ARAKI, HIROYUKI
 ; APPLICANT: HAGIHARA, HIROSHI
 ; APPLICANT: IGARASHI, KAZUAKI
 ; APPLICANT: HAYASHI, YASUHIRO
 ; APPLICANT: OZAKI, KATSUYA
 ; TITLE OF INVENTION: HIGHLY PRODUCTIVE ALPHA-AMYLASES
 ; FILE REFERENCE: 214377USO
 ; CURRENT APPLICATION NUMBER: US/09/971,611
 ; PRIOR FILING DATE: 2001-10-09
 ; PRIOR APPLICATION NUMBER: JP 2000/310605
 ; NUMBER OF SEQ ID NOS: 51
 ; SOFTWARE: PatentIn version 3.1

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; SEQ ID NO 1
; LENGTH: 1786
; TYPE: DNA
; ORGANISM: Bacillus sp. KSM-API378
; FEATURE:
; NAME/KEY: sig peptide
; LOCATION: (155)..(247)
; OTHER INFORMATION:
; NAME/KEY: mat peptide
; LOCATION: (248)..()
; OTHER INFORMATION:
; NAME/KEY: CDS
; LOCATION: (155)..(1702)
; OTHER INFORMATION:
; US-09-971-611-1

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Query Match      100.0%; Score 1776; DB 9; Length 1786;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1776; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 ATTTAAATTTGAATGACCTTATGAAATATGTAAGCATTCGCGACGAGAAAAAC 60
DB 11 ATTTAAATTTGAATGACCTTATGAAATATGTAAGCATTCGCGACGAGAAAAAC 70
QY 61 TTGGAGTTGGAAGGATATTAAGGATTTTGTGACTGTGTGAAAAAGCTTGCAAT 120
DB 71 TTGGAGTTGGAAGGATATTAAGGATTTTGTGACTGTGTGAAAAAGCTTGCAAT 130
QY 121 AAATGAGAGAGAGGCTTTTATGAACTTCAATACCGTAATTAATGCGTACTATTA 180
DB 131 AAATGAGAGAGAGGCTTTTATGAACTTCAATACCGTAATTAATGCGTACTATTA 190
QY 181 ACCTATTTGTAAGTGTGCTGTTTGTTCATATATGACGAGAACGAGAACGCCAT 240
DB 191 ACCTATTTGTAAGTGTGCTGTTTGTTCATATATGACGAGAACGAGAACGCCAT 250
QY 241 CATTAATGAGAGAGGAGCATGATGATGATGATGATGATGATGATGATGATGATG 300
DB 251 CATTAATGAGAGAGGAGCATGATGATGATGATGATGATGATGATGATGATGATG 310
QY 301 AACCACTGGAACAGGTTACGAGATGACGACGCTAATTAAGATTAAGGATTTAC 360
DB 311 AACCACTGGAACAGGTTACGAGATGACGACGCTAATTAAGATTAAGGATTTAC 370
QY 361 GTTTGATTCCTCTGATGAGAGAGGAGCTTCGCAAAATGATGATGATGATGAT 420
DB 371 GTTTGATTCCTCTGATGAGAGAGGAGCTTCGCAAAATGATGATGATGATGATG 430
QY 421 GATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 480
DB 431 GATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 490
QY 481 AGGAGTCAAGTTGCAAGGTCCTGTAATCTTTGAAAAATTAACGGGATTTCAAG 540
DB 491 AGGAGTCAAGTTGCAAGGTCCTGTAATCTTTGAAAAATTAACGGGATTTCAAG 550
QY 541 GATGTCGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 600
DB 551 GATGTCGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 610
QY 601 GTGAACCGAAGCAACCGAAGCAAGAAATATCAGTGAATATCAGTGAATATCAG 660
DB 611 GTGAACCGAAGCAACCGAAGCAAGAAATATCAGTGAATATCAGTGAATATCAG 670
QY 661 AAATTTGATTTCCCTGGAAGAGAAATATCAGTGAATATCAGTGAATATCAG 720
DB 671 AAATTTGATTTCCCTGGAAGAGAAATATCAGTGAATATCAGTGAATATCAG 730
QY 721 TTGTAAGGAGCAATGAGGATGATGATGATGATGATGATGATGATGATGATGAT 780
DB 731 TTGTAAGGAGCAATGAGGATGATGATGATGATGATGATGATGATGATGATGAT 790
QY 781 GTTACCGGAAAGGAGGATGAGGATGATGATGATGATGATGATGATGATGATGAT 840

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DB 791 GGTACCGGAAAGGAGGAGGATGAGGATGATGATGATGATGATGATGATGATGAT 850
QY 841 ATGTATGCAACATTTATATGATGATGATGATGATGATGATGATGATGATGATG 900
DB 851 ATGTATGCAACATTTATATGATGATGATGATGATGATGATGATGATGATGATG 910
QY 901 GTTTGATTAACAATCAGTGAATGATGATGATGATGATGATGATGATGATGATG 960
DB 911 GTTTGATTAACAATCAGTGAATGATGATGATGATGATGATGATGATGATGATG 970
QY 961 AAATACGCTATACGAGATGAGGATGATGATGATGATGATGATGATGATGATG 1020
DB 971 AAATACGCTATACGAGATGAGGATGATGATGATGATGATGATGATGATGATG 1030
QY 1021 TTGTCAGTTGCAAGATTTTGGAAAAATGACCTTGTGCAATGCAAACTATTA 1080
DB 1031 TTGTCAGTTGCAAGATTTTGGAAAAATGACCTTGTGCAATGCAAACTATTA 1090
QY 1081 ACAAGTTGGAATCAGTCCGCTGATGATGATGATGATGATGATGATGATGATG 1140
DB 1091 ACAAGTTGGAATCAGTCCGCTGATGATGATGATGATGATGATGATGATGATG 1150
QY 1141 AATAGTGTGCTATTTTGTATGAGAAATATTTAAATGTTCTGTGACAAAAAC 1200
DB 1151 AATAGTGTGCTATTTTGTATGAGAAATATTTAAATGTTCTGTGACAAAAAC 1210
QY 1201 CCTATACATGACGATCAGTGTGATGATGATGATGATGATGATGATGATGATG 1260
DB 1211 CCTATACATGACGATCAGTGTGATGATGATGATGATGATGATGATGATGATG 1270
QY 1261 TCCTTTGTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1320
DB 1271 TCCTTTGTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1330
QY 1321 GGTATCCCTTCCGTAATTTAAGGATGATGATGATGATGATGATGATGATGAT 1380
DB 1331 GGTATCCCTTCCGTAATTTAAGGATGATGATGATGATGATGATGATGATGAT 1390
QY 1381 ATGAAATCTTAAATTTGATGATGATGATGATGATGATGATGATGATGATGAT 1440
DB 1391 ATGAAATCTTAAATTTGATGATGATGATGATGATGATGATGATGATGATGAT 1450
QY 1441 CATGATTTATTTGATGATGATGATGATGATGATGATGATGATGATGATGATG 1500
DB 1451 CATGATTTATTTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1510
QY 1501 CCAAAATTCAGGACTTGCACATATATGTCGATGAGGCTCAGGGGATTAAT 1560
DB 1511 CCAAAATTCAGGACTTGCACATATATGTCGATGAGGCTCAGGGGATTAAT 1570
QY 1561 GTGCGGAAACATTAACCTGCGCAAGTATGAGAGATATCAACCGGAAATG 1620
DB 1571 GTGCGGAAACATTAACCTGCGCAAGTATGAGAGATATCAACCGGAAATG 1630
QY 1621 GTCAACATTAATCAGATGATGATGATGATGATGATGATGATGATGATGAT 1680
DB 1631 GTCAACATTAATCAGATGATGATGATGATGATGATGATGATGATGATGAT 1690
QY 1681 TGGGTGAAGCAATTAATTAAGAAACAAGAGCGAAAAATTAATCTTCTTA 1740
DB 1691 TGGGTGAAGCAATTAATTAAGAAACAAGAGCGAAAAATTAATCTTCTTA 1750
QY 1741 CCGATCACTCATACCCCAATTAATTAATTTGGAAGCTT 1776
DB 1751 CCGATCACTCATACCCCAATTAATTAATTTGGAAGCTT 1786

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RESULT 4
US-10-798-278-1
; Sequence 1, Application US/10798278
; Publication No. US20040265959A1
; GENERAL INFORMATION:

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APPLICANT: ARAKI, HIROYUKI
APPLICANT: ENDO, KEIJI
APPLICANT: HAGIHARA, HIROSHI
APPLICANT: IGARASHI, KAZUAKI
APPLICANT: HAYASHI, YASUHIRO
APPLICANT: OZAKI, KATSUYA
TITLE OF INVENTION: HIGHLY PRODUCTIVE ALPHA-AMYLASES
FILE REFERENCE: 214377USO
CURRENT APPLICATION NUMBER: US/10/798,278
PRIOR APPLICATION NUMBER: US/09/971,611
PRIOR FILING DATE: 2001-10-09
PRIOR APPLICATION NUMBER: JP 2000/310605
PRIOR FILING DATE: 2001-10-11
NUMBER OF SEQ ID NOS: 51
SOFTWARE: PatentIn version 3.1
SEQ ID NO: 1
LENGTH: 1786
TYPE: DNA
ORGANISM: Bacillus sp. KSM-AP1378
FEATURE:
NAME/KEY: sig_peptide
LOCATION: (155)..(247)
OTHER INFORMATION:
FEATURE:
NAME/KEY: mat_peptide
LOCATION: (248)..()
OTHER INFORMATION:
FEATURE:
NAME/KEY: CDS
LOCATION: (155)..(1702)
OTHER INFORMATION:
US-10-798-278-1

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Query Match 100.0%; Score 1776; DB 18; Length 1786;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1776; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 ATATTAATTTGAATGAACACCTATGAAATATGTTGACGATGGCGACGAGAAAC 60
DB 11 ATATTAATTTGAATGAACACCTATGAAATATGTTGACGATGGCGACGAGAAAC 70
QY 61 TTGGAGTTAGAGAGTGAATATTAAGATTTTGTGCTGTGAAACGCTTGCAAT 120
DB 71 TTGGAGTTAGAGAGTGAATATTAAGATTTTGTGCTGTGAAACGCTTGCAAT 130
QY 121 AAATGAAGAGAGGCTCTTTTATGAACCTCAATACCGTATATTAGGCTACTATTA 180
DB 131 AAATGAAGAGAGGCTCTTTTATGAACCTCAATACCGTATATTAGGCTACTATTA 190
QY 181 ACATATTGTTAGCTGTAGCTGTTTGTTCATATATGACGAAACGACACAGCCCAT 240
DB 191 ACATATTGTTAGCTGTAGCTGTTTGTTCATATATGACGAAACGACACAGCCCAT 250
QY 241 CATATGGAGAGATGGAGACCATGATGATTTTGAATGGCATTTGCCAATGACGGG 300
DB 251 CATATGGAGAGATGGAGACCATGATGATTTTGAATGGCATTTGCCAATGACGGG 310
QY 301 AACCACTGGAACAGGTTACGAGATGACGAGCTTAATTAAGATTAAGAGGATTAACGCT 360
DB 311 AACCACTGGAACAGGTTACGAGATGACGAGCTTAATTAAGATTAAGAGGATTAACGCT 370
QY 361 GTTTGATTTCTCTGTCATGAGAGGGAATTCGCAAAATGATGTTGGTATGTCCTAT 420
DB 371 GTTTGATTTCTCTGTCATGAGAGGGAATTCGCAAAATGATGTTGGTATGTCCTAT 430
QY 421 GATTGTGAGATCTTGTGAGATTTAACCAAAAGGGAACCGTCCGTAACAAATATGAGCA 480
DB 431 GATTGTGAGATCTTGTGAGATTTAACCAAAAGGGAACCGTCCGTAACAAATATGAGCA 490
QY 481 AGGAGTCAGTTGCAAGGTGCGGTGACATCTTTGAAAAATTAACGGGATTCAGATTATGGG 540
DB 491 AGGAGTCAGTTGCAAGGTGCGGTGACATCTTTGAAAAATTAACGGGATTCAGATTATGGG 550

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QY 541 GATGTCGTATGATCATTAAGTGTGACAGACGGGACAGAGATGTTAATGCGGTGGA 600
DB 551 GATGTCGTATGATCATTAAGTGTGACAGACGGGACAGAGATGTTAATGCGGTGGA 610
QY 601 GTGAACCGAAGCAACCGAAGCAAGAAATATCAGGTGATATACCATTTGAAGCATGACG 660
DB 611 GTGAACCGAAGCAACCGAAGCAAGAAATATCAGGTGATATACCATTTGAAGCATGACG 670
QY 661 AAATTTGATTTCCCTGGAAGGAAATATCCATTCGAATTTAATGCGGTGATCAT 720
DB 671 AAATTTGATTTCCCTGGAAGGAAATATCCATTCGAATTTAATGCGGTGATCAT 730
QY 721 TTTGATGGAGCAGATTGGGATCAGTCAGCTGCTGAGAACAAATATTAATTCAGA 780
DB 731 TTTGATGGAGCAGATTGGGATCAGTCAGCTGCTGAGAACAAATATTAATTCAGA 790
QY 781 GGTAACCGAAGGAGATGGGACTGGGAAGTAGATATAGAAACGGCACTATGATTCCTT 840
DB 791 GGTAACCGAAGGAGATGGGACTGGGAAGTAGATATAGAAACGGCACTATGATTCCTT 850
QY 841 ATGATGAGCAGATTGATATGATATCAGATCAGAGATTAATCAATTAAGAAATTTGGGA 900
DB 851 ATGATGAGCAGATTGATATGATATCAGATCAGAGATTAATCAATTAAGAAATTTGGGA 910
QY 901 GTTTGATTAACAATTAACAATTAATCTAGATGATTTAATGATGATGCTGGAACATATT 960
DB 911 GTTTGATTAACAATTAACAATTAATCTAGATGATTTAATGATGATGCTGGAACATATT 970
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DB 1031 TTTGACGTTGAGAAATTTTGAAGAAATGACCTTGTGCAATTCGAAATATTAATTA 1090
QY 1081 ACAAGTTGAGTCACTCCGCTGCTGATGCTCTGCTCAATTAATTTGATTAACAATGATCT 1140
DB 1091 ACAAGTTGAGTCACTCCGCTGCTGATGCTCTGCTCAATTAATTTGATTAACAATGATCT 1150
QY 1141 AATAGTGTGCTATTTTGTATATGAGAAATATTTAATGTTCTGTGTAACAAACAC 1200
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DB 1211 CCTATACATGACATGATTTGTTGATACCATATCTCTACGCCAGAGAAAGCATGGAA 1270
QY 1261 TCCCTTTGTTCAATGCTGTTCAACCACTGGCATATGATTTGTCGAAAGGAGCA 1320
DB 1271 TCCCTTTGTTCAATGCTGTTCAACCACTGGCATATGATTTGTCGAAAGGAGCA 1330
QY 1321 GATTACCTTCCGATATTTTACGATATTAATCAAGGATTAATCAATGATGTTCTTTCG 1380
DB 1331 GATTACCTTCCGATATTTTACGATATTAATCAAGGATTAATCAATGATGTTCTTTCG 1390
QY 1381 ATGAATCTAAATATGATCACTTCTGACAGGACGTCAAACGATATGCTTACGGAACCAA 1440
DB 1391 ATGAATCTAAATATGATCACTTCTGACAGGACGTCAAACGATATGCTTACGGAACCAA 1450
QY 1441 CATGATTTATTTGATCATATGATATTAATGCTGCTGACAGAGAGGAGACAGCTCCAC 1500
DB 1451 CATGATTTATTTGATCATATGATATTAATGCTGCTGACAGAGAGGAGACAGCTCCAC 1510
QY 1501 CCAATTTACAGGACTTGCAACTATATGTCGATGAGGACAGGGGGTAAATTAATGATGAT 1560
DB 1511 CCAATTTACAGGACTTGCAACTATATGTCGATGAGGACAGGGGGTAAATTAATGATGAT 1570
QY 1561 GTGCGGAAACATTAAGCTGCGCAAGATGAGAGATATCACCGGAAATAGGTTCTGTATCC 1620
DB 1571 GTGCGGAAACATTAAGCTGCGCAAGATGAGAGATATCACCGGAAATAGGTTCTGTATCC 1630

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Db	301	GGTGAATGCGTCATGAAATCATTAAGGTGGAGCAGATGGTACGGAATTGTAAATGCGGTA	360
Qy	598	GAAGTGAACCGAGCAACCGAAACCGAAGAAATATCAGTGAATACACCATTTGAAGCATGG	657
Db	361	GAAGTGAATCGAGCAACCGAAACCGAAGAAACCTCAGAGAGTATGCAATGGAAGCCGTGG	420
Qy	658	ACGGAATTGATTTCCCTGGAAAGGAAATPACCATTTCCAACTTTAAATGGCCGTGAT	717
Db	421	ACAAAGTTGATTTTCTTGAAAGGAAATPACCATTTCCAGCTTTAAAGTGGCCGTGAT	480
Qy	718	CATTTGATGGGACAGATTGGGATCAGTCACTGACGCTTCAGAACAAATATATTAATTC	777
Db	481	CATTTGATGGGACAGATTGGGATCAGTCACTGACGCTTCAGAACAAATATATTAATTC	540
Qy	778	AGAGGTACCGGAAAGCATTGGGACTGGGAAGTAGATATPAGAAACGGCACTATGATTAC	837
Db	541	AGGGGAACAGGCAAGCCCTGGGACTGGGAAGTGCATACAGAAATGGCAACTATGACTAT	600
Qy	838	CTTATGTATGAGACATTTGATATGGAATCATCCAAAGTAATCAATGAACTTAGAAATTGG	897
Db	601	CTTATGTATGAGACGTGATATGGAATCACCAAAGTAATCAATGAACTTAGAAACTGG	660
Qy	898	GGAGTTTGATATCAAAATACCTTAATCTAGATGAATTTAGAAATCGATGCTGTAACAT	957
Db	661	GGAGTGTGATATGGAATACCTTAATCTAGATGAATTTAGAAATCGATGCTGTAACAT	720
Qy	958	ATTAAATACAGCTATACGAGAGATTGGCTTAACATGTGCGTAAACACCAAGTAAACA	1017
Db	721	ATAAAATATAGCTTTACGAGAGATTGGCTTAACATGTGCGTAAACACCAAGTAAACA	780
Qy	1018	ATGTTTGCAGTGGAGAAATTTTGGAAAAAGACCTTGCTGCAATCGAAACATATTTAAT	1077
Db	781	ATGTTTGCAGTGGAGATTTTGGAAAAAGACCTTGCTGCAATCGAAACATATTTAAT	840
Qy	1078	AAACAGATGGGAATCACTCCGTTTGATGATTTCTCTTCAATTAATTTGTACATGCA	1137
Db	841	AAACAGATGGGAATCACTCCGTTTGATGATTTCTCTTCAATTAATTTGTACATGCA	900
Qy	1138	TCTAATAGTGGCTATTTTGATATGAGAAATATTTAAATGGTCTGTGTCACAAA	1197
Db	901	TCTAATAGCGGTATTTATGATATGAGAAATATTTAAATGGTCTGTGTCACAAA	960
Qy	1198	CACCTTATACATGACATCACTTTGTTGATPACATGACTTCAGCCAGAGAAAGCATTG	125
Db	961	CATCAACACATGCGCTTACTTTGTTGATPACATGATTCAGCCCGGGAAAGCATTTG	1020
Qy	1258	GAATCCATTGTTCAATGSGTGTCAAAACCACTGGCATATGATGATTCTGACAAAGGAG	131
Db	1021	GAATCCATTGTTCAACATGSGTGTCAAAACCACTGGCATATGATGATTCTGACAAAGGAG	108
Qy	1318	CAAGTTACCCCTCCGATATTTTACGATGATTACTACGGTATACCACTCATGGTTCCT	137
Db	1081	CAAGTTATCCCTCCGATATTTTATGGGAGTTACTACGGTATCCCAACCATGGTTCCTG	114
Qy	1378	TCGATGAATCTAAATATTGATCACTTCTGACGAGCATCAACGATATGCTACGGAAC	143
Db	1141	GCTATGAATCTAAATATGACCCCTTCTGACGAGCATCAACCTTTTGCCATATGATACG	120
Qy	1438	CAATATATTAATTTGATCATGATATTAATGCGCTGGAGAGAGAAAGGGGACAGCTCC	149
Db	1201	CAGATATTAATTTGATCATGATATTAATGCGTGGAGACAGAGAGGGGAAATATGCTCC	126
Qy	1498	CACCAAAATTCAGACCTTGCAACTATTAATGTCATGGGCCAGGGGGGTAAATTAATGATG	155
Db	1261	CATCAAAATTCAGGCCCTTGCCACATATATATGTCATGATGTCAGGATGGTAAACAAATGATG	132
Qy	1558	TATGTGCGGAAACATAAAGCTGGCCAGATATGAGAGATATCACCGGAAATATGCTGTGT	161
Db	1321	TATGTGCGGAAATTAAGCGGGGCAAGATTGAGAGATATTAACCGGAAATATGACAGGC	138
Qy	1618	ACGTCACCAATATGACATGTTGGGGGAATTCACCTGTAACCGAGGGGCAGTTTCG	167

Db 1381 ACCGACAAATTAAAGCAGACGAGATGGGTTATTTCTCTTTAATGAGAGGTCCTTGG 1444

QY 1678 GTTTGGGTGAAGCAATAA 1695

Db 1441 GTTTGGGTGAAGCAATAA 1458

RESULT 7

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US-09-769-864-9
: Sequence 9, Application US/09769864
: Patent No. US20010039253A1
: GENERAL INFORMATION:
: APPLICANT: Borchert, Torben V.
: APPLICANT: Svendsen, Allan V.
: APPLICANT: Andersen, Carsten
: APPLICANT: Nielsen, Bjarne
: APPLICANT: Nissen, Torben L.
: APPLICANT: Kjaerulff, Soren
: TITLE OF INVENTION: Alpha-Amulase Mutants
: FILE REFERENCE: 5366-200-US
: CURRENT APPLICATION NUMBER: US/09/769,864
: CURRENT FILING DATE: 2001-01-25
: PRIOR APPLICATION NUMBER: 09/183,412
: PRIOR FILING DATE: 1998-10-30
: NUMBER OF SEQ ID NOS: 58
: SOFTWARE: FastSeq for Windows Version 3.0.
: SEQ ID NO 9
: LENGTH: 1455
: TYPE: DNA
: ORGANISM: Bacillus
US-09-769-864-9

```

Query Match	65.7%	Score 1167	DB 9	Length 1455
Best Local Similarity	87.6%	Pred. No. 4e-302		
Matches 1275; Conservative	0	Mismatches 180	Indels 0	Gaps 0

QY	238	CATCATTAATGGGACCAATGGAGCACTGATGCAGTATTTTGGATGGCATTTGGCCAATGAC	297
Db	1	CATCATTAATGGAAACAATGGTACTATGATGCAATTTTGGATGGTATTTGGCCAATGAC	60
QY	298	GGGAAACCACTGGAAACAGGTTACGAGATGACGACGTTAACTTAAAGATGAAAGGATTACC	357
Db	61	GGGAATCAATTGGAAACAGGTTAGGGATGACGACGTTAACTTAAAGATGAAAGGATTAAACA	120
QY	358	GCTGTTTGGATTTCCCTCGTCATGGAAGGGGAACTTCGCAAAATGATGTTGGGTATGATGCC	417
Db	121	GCTGATATGATATCCACCTGTCATGGAAGGGGAACTTCGCAATGATGATGTTATGAGACC	180
QY	418	TATGATTTTGTAACGATCTTGATGGATTTTAAACCAAAAGGAAACCGTCGTACAAATATGAGC	477
Db	181	TATGATTTTATATGATCTTGAGAGATTTTAAACGAAAGGGACGGTTCGTACAAATATGAGA	240
QY	478	ACAAGGATTCAGTTCGCAAGTGCCTGACATCTTTGGAAAAATTAACGGATTCACATTTAT	537
Db	241	ACACGCCAACAGCTACAGAGCTGCGGTGACCTCTTTAAAAAATTAACGGCAATTCAGGTATAT	300
QY	538	GGGAGTGTCTGATGTAATCATTAAGTGGAGAGACAGGACAGAGATGGTAAATCCGGTG	597
Db	301	GGTATGTCTGTCATGATATCATTAAGTGGAGAGATGGTATCGGAATTTGTAAATCCGGTA	360
QY	598	GAAGTGAACCGAAGCACCGAAACCAAGAAATATCAGGTGAATACACCAATTGAAGCATGG	657
Db	361	GAAGTGAATCCGAGCGAACCCGAAACCGAGAAACCTCAGAGAGATGACAAATGAAACGTGG	420
QY	658	ACGAAATTTGATTTTCCCTGGAAAGAGAAATACCCATTTCCACTTTAAATGGCGCTGGTAT	717
Db	421	ACAAAGTTTGATTTTCCCTGGAAGAGAAATTAACATTCAGCTTTTAAAGTGGCGCTGGTAT	480
QY	718	CATTTTGTGGAGACGATTTGGATCAGTCAAGTCAGCTTCAGAAACAATAATATATAATTC	777
Db	481	CATTTTGTGGAGACGATTTGGATCAGTCAAGTCAGCTTCAGAAACAATAATATATAATTC	540
QY	778	AGAGGTACCGAAGAGCATGGGACTGGGAAGTAGATATAGAGAACGGCAACTATGATTAAC	837

Db	541	AGGGGAACAGGCCAAGCCTGGGACTGGGAATCGATACAGAAATGGCAACTATGACAT	600
Oy	838	CTTATGTATGCAACATTTGATATGATCATCCAGAATATCAATGAACCTTAGAAATTGG	897
Db	601	CTTATGTATGACAGCGTGATATGATCACCCAAGTAATACATGAACCTTAGAAACTGG	660
Oy	898	GGAGTTTGGTATACAAATACACTTAATCTAGATGATTTAGAAATCGATGCTGTGAAACAT	957
Db	661	GGAGTGTGTATACGAATACACTGAACCTTGATGATTTAGAAATATGATGCACTGAAACAT	720
Oy	958	ATTAAATACAGCTATACGAGAAATTTGGCTAACACATGTGCTAACACCAAGTAAACCA	1017
Db	721	ATTAAATATACCTTTACGAGAAATTTGGCTTACATGTGCTAACACCAAGTAAACCA	780
Oy	1018	ATGTTTGCAGTTGAGAAATTTTGGAAAAATGACCTTGCTGAATCGAAACATATTTAAT	1077
Db	781	ATGTTTGCAGTGTGAGTTTGGAAAAATGACCTTGCTGAATGAAACATATTTGAT	840
Oy	1078	AAACAAGTTTGAATCACTCCGTTTCGATGTTTCTCTCATTTTAAATTTTACATGCA	1137
Db	841	AAACAAGTTTGAATCACTCGTGTGTTGATTTCTCTCCCATTAATTTTACATGCA	900
Oy	1138	TCATAATGTGTGCTATTTTGTATATGAGAAATATTTAAATGTTCTGTGTCACAAA	1197
Db	901	TCATAATGCGGTGTTTATATGATATGAAATTTTAAATGTTCTGTGTGCAAAA	960
Oy	1198	CACCCATACATGAGTACAAATTTTGTATACATACATCTGACCGAGGAAGCATTG	1257
Db	961	CATCAACACATGCGCTTACTTTTGTATACATGATTTCTGACCGGGGAAGCATTG	1020
Oy	1258	GAATCCTTTTGTTCATCGTGTGTTCAAAACAATGCGATATGATGATTTCTGACAAGGAG	1317
Db	1021	GAATCCTTTTGTTCACAATGTTTAAACCACTTGATATGATTTGTTCTGACAAGGAA	1080
Oy	1318	CAAGTTTACCTTCGGTATTTTACGTTGATTACTACGATATACCACTCATGTGTTCT	1377
Db	1081	CAAGTTTATCCTTCGGTATTTTATGGGGATTACTACGATTAACCAACCAATGATGTTCCG	1140
Oy	1378	TCGATGAAATCTAAATTTGATCCACTTCTGAGGCAAGTCAAAAGTATGCTACGGAAC	1433
Db	1141	GTATGAAATTTAAATATGACCCCTTCTGACAGCAAGTCAAACTTTTGCTTATGTATCG	1200
Oy	1438	CAACATGATTAATTTTGTATCATCATGATATTAATCGGCTGACGAGAGAAAGGGAACA	1497
Db	1201	CAGATGATTAATTTTGTATCATCATGATATTAATCGGTTGACAAAGAGGGAATATGCTCC	1260
Oy	1498	CACCCAAATTCAGACCTTGCAACTATTAATGTCCATGTGGCCAGGGCGTAAATATGATG	1557
Db	1261	CATCCAAATTCAGGCTTGGCCACCATTAATGTCAATGATGCTCAGGATGTGTAACAAATGATG	1320
Oy	1558	TATGTGCGGAAACATAAAGCTGCGCAAGTATGAGAGATATCACCGGAAATAGGCTTG	1617
Db	1321	TATGTGCGGAAATATTAAGCGGACAACTTTGAGAGATATTAACCGGAAATAGGACAGGC	1380
Oy	1618	ACCGTCAACATTAATGACATGTGTTGGGGGAATTTCACTGTAACGAGGGGCAAGTTTCG	1677
Db	1381	ACCGTCAACATTAATGACAGCGATGGGGTAATTTCTGTTAATGAGGGGCTCGGTTTCG	1440
Oy	1678	GTTTGGGTGAAGCA 1692	
Db	1441	GTTTGGGTGAAGCA 1455	

RESULT 8

US-09-769-864-13
Sequence 13, Application us/09769866
Patent No. US20010039253A1
GENERAL INFORMATION:
APPLICANT: Borchert, Torben V.
APPLICANT: Svendsen, Allan
APPLICANT: Andersen, Carsten
APPLICANT: Nielsen, Blarne

QY	238	CATCATATATGGGACGAATGGGACCAATGACATATTTGAAATGGCATTTGGCAATATAC	297
Db	1	CATCATATATGGACCAAAATGCTATCTATGATGCAATTTTGGATATTTGGCAAAATGAC	60
QY	298	GGGAACCACTGGAAACGGTTACCGAGATGACCGACGTTAACTTTAAAGATPAAAGGATTAAC	357
Db	61	GGGAATCATTTGGAAACAGGTTGAGGGATGACCGACGTTAACTTTAAAGATPAAAGGATTAACA	120
QY	358	GCTGTTTGGAAATTCCTCTCGCATGGAAGGGGACTTGGCAAAATGATGTTGGGTATGTGTGCC	417
Db	121	GCTGATATGGAATCCCACTCGCATGGAAGGGGAACTTCCAGAAATGATGATGAGTTATGGAACCC	180
QY	418	TATGATTTGTATCGAATCTTGTTGATGTTTAAACAAAAGGAAACCGTCCGTACAAAATATGAC	477
Db	181	TATGATTTTATATGATCTTGAGAGATTTTAAACGAAGGGGACGGTTCGTACAAAATATGGA	240
QY	478	ACAAGAGACTCAGTTGCAAGGTGCCGTGCATCTTTGAAAATATACGGGATTTCAAGTTTAT	537
Db	241	ACAAGCAACCAAGTACAGGCTGCGGTGACCTCTTTAAAAAATATACGGCATTTCAAGTATAT	300
QY	538	GGGATATCTGTGATGTAATCATTTAAAGTGTGACAGACGGGACAGAGATGTATATCCGCTG	597
Db	301	GGTATATCTGTATGAAATCATTTAAAGTGTGAGAGATGTATGCGAAATTTGTATATCCGCTA	360
QY	598	GAAGTGAACCGAGCAACCGAAACCAAGAAATATATCAGGTGAATACCACTTGAAGACATGG	657
Db	361	GAAGTGAATCGAGCAACCGAAACCAAGAAACCTGAGAGATATGCAATATGAACCGCTGG	420
QY	658	ACGAAATTTGATTTCCCTGGAAGAGAAATACCCATTTCCAACTTTTAAATGGCGCTGTAT	717
Db	421	ACAAAGTTGATTTTCCCTGGAAGAGAAATATACCACTTCCAGCTTTAAATGGCGCTGTAT	480
QY	718	CATTTTGAATGGGACAGATTTGGGATGATGACAGTCAAGCTTCACGAACAAATATATTAATTC	777
Db	481	CATTTTGAATGGGACAGATTTGGGATGATGACAGCTTCACGAACCAAAATATATTAATTC	540
QY	778	AGAGTACCGGAAAGGCATGGGACTGGGAGATGATATAGAAACGGCAACATATGATATAC	837
Db	541	AGGGGAACGGCAACGGCTCTGGGACTGGGAATGTCATACAGAGAAATGGCAACTATATACAT	600
QY	838	CTTATATGATGAGACATTGATATGATGATCATCCAGAAATGTAATCAATGAACTTAGAAATGG	897
Db	601	CTTATATGATGAGACAGTGGATATGATATCACCCAGAAATGTAATCAATGAACTTAGAAATCGG	660
QY	898	GGAGTTTGGTATACAAATACCTTAATCTTAAGTGAATTTAGAAATGAGATGACAGTGAACAT	957
Db	661	GGAGTGTGTATACAAATACCTGAACCTTGAATGATTTAGAAATGAGATGACAGTGAACAT	720
QY	958	ATTAAATACAGCTATACAGAGATTTGGCTTAAACAACATGTGCTTAAACACACAGAGTAAACCA	1017
Db	721	ATTAAATATATACCTTTACAGAGATTTGGCTTACACATGTGCTTAAACACACAGATTAACCA	780
QY	1018	ATGTTTGACGTTGCAGAAATTTTGGAAAAATGACCTTGCTGCATACGAAAAACATATTTAAT	1077

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1 Patent NO US20020068352A1
2
3 GENERAL INFORMATION:
4 APPLICANT: No. US20020068352A1Ozymes A/S
5 APPLICANT: Svendsen, Allan
6 APPLICANT: Jorgensen, Christel Thea
7 APPLICANT: Nielsen, Bjarne Ronfeldt
8 TITLE OF INVENTION: Alpha-amylase variants with altered 1,6 activity
9 FILE REFERENCE: 6140..200-US
10 CURRENT APPLICATION NUMBER: US/09/854,346
11 CURRENT FILING DATE: 2001-05-11
12 NUMBER OF SEQ ID NOS: 15
13 SOFTWARE: PatentIn version 3.1
14 SEQ ID NO 1
15
16 LENGTH: 1455
17
18 TYPE: DNA
19
20 ORGANISM: Bacillus sp.
21
22 FEATURE:
23 NAME/KEY: CDS
24 LOCATION: (1)..(1455)
25
26 OTHER INFORMATION: SP690
27
28 US-09-854-346-1

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	Query Match	85.7%;	Score 1167;	DB 9;	Length 1455;	
	Best Local Similarity	87.6%;	Pred. No. 4e-302;			
	Matches 1275;	Conservative	0;	Mismatches 180;	Indels	0; Gaps 0;
Qy	238	CATCATAA	TGGGACGAATGGAGCCACATGATGTAATTTGATGTGCATTGCCAATTCAC	297		
Db	1	CATCATATA	TGGAACCAATATGTTACTATATGATGCAATATTTTGCATATGGTATTTTCCCAAATGAC	60		
Qy	298	GGGAACCA	CTTGGAACAGGTTTACGATGATACCGACGTATCTTAAAAGATPAAAGGGATTAAC	357		
Db	61	GGGAATC	ATTGGAAACAGGTTGAGGGATGACGACGTATCTTAAAAGATPAAAGGGATTAACA	120		
Qy	358	GCTGTTTT	GATTTTCCTCTCTGCATGGAAGGGACCTTGC AAAATGATGTTGGTATGTCGC	417		
Db	121	GCTGATGAT	TCCCACCTCGCATGGAAGGGGACTTCCAGATGATGATGATTAAGGACC	180		
Qy	418	TATGATTT	GTATACATCTTGTGTGAGTTTAAACAAAAGGGAACCCGTCGTAACAAATATGAC	477		
Db	181	TATGATTT	ATATATATGATCTTGTGAGATTTTAAACGAAAGGGAGCGTTGTAACAAATATGGA	240		
Qy	478	ACAAGA	GTACAGTTGCAAGTGCCGTGCATCTTTGAAAAATTAACGGGATTC AAGTTAT	537		
Db	241	ACAOSCA	ACACAGCTACAGGCTGCGGTGACCTTTAAAAATTAACGGCATT CAGGTATAT	300		
Qy	538	GGGATG	TCTGTATGATCATTAAGSTGGAGACACGGGACAGAGATGTGTAATATGCGGTG	597		
Db	301	GGTATG	TGTCATCAATCATTAAGSTGGAGACAGATGTGTACGGAATTTGTAATGCGGTA	360		
Qy	598	GAAATGA	CCGAAGCACCCGAAACCAAGAAATATACAGSTGAAATACACATTGAAGCATGG	657		
Db	361	GAAATGA	ATTCGGAGCACCCGAAACCGAATTAACCTCAGAGATATGCAATGAAACGCTGG	420		
Qy	658	AAGAAAT	TGATTTCCCTGGAAGAGAAATVACCATTCOAACCTTAAATGCGCTGTAT	717		
Db	421	ACAAAGT	TGATTTTCTCTGGAAGAGAAATVAAACATTCAGCTTAAATGCGCTGTAT	480		
Qy	718	CATTGTA	NGGGACAGATTGGGATGATCAAGTCAGCTTCAGAACAAATATATTAATTC	777		
Db	481	CATTGTA	NGGGACAGATTGGGATGATCAAGTCAGCTTCAGAACAAATATATTAATTC	540		
Qy	778	AGAGGTAC	CGGAAGGCAATGGGACTGGGAAGTAGATATATAGAAACGGCACTATGATTAAC	837		
Db	541	AGGGGAA	CAGGGAAAGCCCTGGGACTGGGAAGTCGATACAGAAATGGCACTATGATAT	600		
Qy	838	CTTATGT	ATGCAGACATTGATATGATCATCCAGAAATATATCAATGAACCTTAGAAATGG	897		
Db	601	CTTATGT	ATGCAGAGCTGGATATGATCAACCGAAGATTAATCAATGAACCTTAGAAATGG	660		
Qy	898	GGAGTTG	GTATACAAATACATCTTATCTAGATGATTTAGAAATGAGTGTGTGAAACAT	957		
Db	661	GGAGTGT	GTATACAAATACATCTTATCTAGATGATTTAGAAATGAGTGTGTGAAACAT	720		
Qy	958	ATTAAAT	ACGCTATACGAGAGATTGGCTAACATGTGCGTTAACACACAGGTAAACCA	1017		
Db	721	ATAAATAT	ATAGCTTTATACGAGATTTGGCTTAACATGTGCGTTAACACACAGGTAAACCA	780		
Qy	1018	ATGTTGA	GTGAGTGGAAATTTTGGAAAAATGACTTGTGCAATCGAATACTATTTAAT	1077		
Db	781	ATGTTGA	GTGAGTGGCTGAGTTTGGAAAAATGACTTGTGCAATTTGAAAATCTATTTGAT	840		
Qy	1078	AAAAACA	AGTTGGAACTCTCGGTGTGATGTTCCTCTTCAATTAATTTTGTACATGCA	1137		
Db	841	AAAAACA	AGTTGGAACTCTCGGTGTGATGTTCCTCTTCAATTAATTTTGTACATGCA	900		
Qy	1138	TCTAAT	ATGTTGGCTATTTTGAATNGAAATATTTTAAATGTTCTGTGCTGTAACAAA	1197		
Db	901	TCTAAT	ATGTTGGCTATTTTGAATNGAAATATTTTAAATGTTCTGTGTGTAACAAA	960		
Qy	1198	CACCTTA	TATACGACATTTTGTGTAATCAATGACTCAGACCCAGAGAAACATTTG	1257		
Db	961	CATCCA	ACAGATCCGTTATCTTTGTGTAATCAATGATCTCAGACCCGGGGAACATTTG	1022		
Qy	1258	GAATCTT	GTGTAATCGTGTGTAACCACTGGCATATGATGATTTCTGACAAAGGAG	1317		

Db	1021	GAATCTCTTGTTCAACAATGGTTAAACCACTTCATATGCATGTGTTTCACAAAGGAA	1080
Qy	1318	CAAGTTTACCCTTCCGTAATTTTACGGGATTACTAAGGTATACCAACTCATGSGTTCCCT	1377
Db	1081	CAAGTTATCTCTTCGTAATTTTAAAGGGATTACACAGGTATCCCAACCAAGTGTTCCG	1140
Qy	1378	TTCGATGAAATCTAAATTTGATTCACCTTCGACGACAGTCAAAAGTATGCTTACGSAAC	1437
Db	1141	GCATAGAAATCTAAATTAAGACCCCTCTTCGACGACAGTCAAACTTTTGCTTAGTGTACG	1200
Qy	1438	CAACATGATTTATTTTGATTCATCATGATATTTATCCGCTGACGAGAGAAGGGAACGCTCC	1497
Db	1201	CAGATGATTTACTTTGATTCATCATGATATTTATCGGTTGGACAAGAGAGGAAATVAGCTCC	1260
Qy	1498	CACCCAAATTCAGACCTTGCAACTATTTATGTCCGATGGGCCAGGGCGGTATTAATTCGATG	1557
Db	1261	CATCCAAATTCAGGCTTCGCCACCATTAATGTCAGATGGTCCAGGTGTGTAAACAAATGATG	1320
Qy	1558	TATGTCCGGAAACATAAAGCTGGCCAAGTATGAGAGATATCAACCGGAAATAGGTGGCT	1617
Db	1321	TATGTGGGGAAAAATTAAGCGGGACAAGTTTGGAGAGATATTTACCGGAAATPAGACAGGC	1380
Qy	1618	ACCGTACCATTAATGACGATGTTGGGGCAATTTCACTGTAAACGAGGGGCGCATTTCCG	1677
Db	1381	ACCGTACCAATTAATGACAGCGATGGGGTATTTCTGTGTTAATGAGAGGCTCCGTTTCG	1440
Qy	1678	GTTTGGGTGAAGCAA 1692	
Db	1441	GTTTGGGTGAAGCAA 1455	

RESULT 10
 US-09-902-188A-4
 ; Sequence 4, Application US/09902188A
 ; Patent No. US20020098996A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Bisgaard-Frantzen, Henrik
 ; Svendsen, Allan
 ; Borchert, Torben Vedel
 ; TITLE OF INVENTION: AMYLASE VARIANTS
 ; NUMBER OF SEQUENCES: 32
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESS: No. US20020098996A1o No. US20020098996A1disk of No. US20020098996A1
 ; STREET: 405 Lexington Avenue, Suite 6400
 ; CITY: New York
 ; STATE: New York
 ; COUNTRY: U.S.A.
 ; ZIP: 10174-6401
 ;
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.25 (EFO)
 ;
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/902,188A
 ; FILING DATE: 10-Jul-2001
 ; CLASSIFICATION: <Unknown>
 ;
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 09/354,191
 ; FILING DATE: <Unknown>
 ;
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Lambitis, Elias J.
 ; REGISTRATION NUMBER: 33,728
 ; REFERENCE/DOCKET NUMBER: 4318.204-US
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 212 867 0123
 ; TELEFAX: 212 867 0298
 ;
 ; INFORMATION FOR SEQ ID NO: 4:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1455 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single

TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-902-188A-4

Query Match 65.7%; Score 1167; DB 9; Length 1455;
Best Local Similarity 87.6%; Pred. No. 4e-302;
Matches 1275; Conservative 0; Mismatches 180; Indels 0; Gaps 0;

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QY 238 CATCATATGGAAGGATGGAACCATGATGCAATTTTGAATGGCATTTGGCCAAATGAC 297
DB 1 CATCATATGGAACCAATGATGATGATGCAATTTTGAATGGATTTTGGCAATGAC 60
QY 298 GGAACCACTGGAACAGGTTACGAGATGACGAGCTTAATTAAAGATTAAGGATTAAC 357
DB 61 GGAATCATTTGGAACAGGTTAGGATGACGAGCTTAATTAAAGATTAAGGATTAACA 120
QY 358 GCTGTTGGATTCCTCTGATGAGAGGGAATTGCAAAATGATGGTATGGTCC 417
DB 121 GCTGATGATCCCACTGATGAGAGGGAATTCCAGATGATGATGATGATGAGACC 180
QY 418 TATGATTTGATGATCTTGTGATTTAACCAAAAGGAAACCGTCCGTAATAATGAC 477
DB 181 TATGATTTGATGATCTTGTGATTTAACCAAAAGGGAACCGTCCGTAATAATGGA 240
QY 478 ACAAGAGTCAGTGAAGGTCGTCATCTTTGAATAACGGGATTCAGTTAT 537
DB 241 ACAGCAGCAACGCTACAGGCTGCGTACCTTTTAAATAACGGGATTCAGTTAT 300
QY 538 GGGGATGTCGATGATGATTAAGTGAAGGAGCAGAGGAGATGATGATGATGATG 597
DB 301 GGTGATGTCGATGATGATTAAGTGAAGGAGATGATGATGATGATGATGATGATG 360
QY 598 GAATGGAACCAAGCAACCAAGAAATATGAGTGAATACCATTTGAAGCATG 657
DB 361 GAATGGAATCGAGCAACCAAGAAATATGAGTGAATACCATTTGAAGCATG 420
QY 658 ACGAAATTTGATTTCCCTGGAAGAAATACCACTTCAACTTTAATGGCGGTAT 717
DB 421 ACGAAATTTGATTTCCCTGGAAGAAATACCACTTCAACTTTAATGGCGGTAT 480
QY 718 CATTTGATGGAAGATGGAATGATGATGATGATGATGATGATGATGATGATGATG 777
DB 481 CATTTGATGGAAGATGGAATGATGATGATGATGATGATGATGATGATGATGATG 540
QY 778 AGAGATACCGGAAAGCATGGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 837
DB 541 AGGGAACAGGCAAGGCTGGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 600
QY 838 CTATATGATGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 897
DB 601 CTATATGATGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 660
QY 898 GGAATTTGATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAAT 957
DB 661 GGAATTTGATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAAT 720
QY 958 ATTAAATACAGCTATACAGAGATGGAATGGAATGGAATGGAATGGAATGGAAT 1017
DB 721 ATTAAATACAGCTATACAGAGATGGAATGGAATGGAATGGAATGGAATGGAAT 780
QY 1018 ATGTTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 1077
DB 781 ATGTTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 840
QY 1078 AAAACAAGTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1137
DB 841 AAAACAAGTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 900
QY 1138 TCTAATAGTGTGCTATTTTGAATGGAATATTTTAAATGTTCTGTGTCGTA 1197
DB 901 TCTAATAGTGTGCTATTTTGAATGGAATATTTTAAATGTTCTGTGTCGTA 960

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QY 1198 CACCTATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1257
DB 961 CATCAACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1020
QY 1258 GAATTCCTTTGTTCAATGCTGTTCAACCATGCTGCTATGATGATGATGATGATG 1317
DB 1021 GAATTCCTTTGTTCAATGCTGTTCAACCATGCTGCTATGATGATGATGATGATG 1080
QY 1318 CAAGTTACCTGCTGCTATGATGATGATGATGATGATGATGATGATGATGATGATG 1377
DB 1081 CAAGTTACCTGCTGCTATGATGATGATGATGATGATGATGATGATGATGATGATG 1140
QY 1378 TCGATGAATCTAAATGATGATGATGATGATGATGATGATGATGATGATGATG 1437
DB 1141 GCTATGAATCTAAATGATGATGATGATGATGATGATGATGATGATGATGATG 1200
QY 1438 CAACATGATTTATTTGATGATGATGATGATGATGATGATGATGATGATGATG 1497
DB 1201 CAGCATGATTTACTTTGATGATGATGATGATGATGATGATGATGATGATGATG 1260
QY 1498 CACCAATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1557
DB 1261 CATCAATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1320
QY 1558 TATGTCGGAACAATTAAGTGGCAAGTATGAGATGATGATGATGATGATGATGATG 1617
DB 1321 TATGTCGGAACAATTAAGTGGCAAGTATGAGATGATGATGATGATGATGATG 1380
QY 1618 ACCGTACCAATTAATGATGATGATGATGATGATGATGATGATGATGATGATG 1677
DB 1381 ACCGTACCAATTAATGATGATGATGATGATGATGATGATGATGATGATGATG 1440
QY 1678 GTTGGGTGAAGCA 1692
DB 1441 GTTGGGTGAAGCA 1455

```

RESULT 11

US-09-918-543-1
Sequence 1, Application US/09918543
Patent No. US20020155574A1
GENERAL INFORMATION:
APPLICANT: No. US20020155574A1ozymes A/S
APPLICANT: Thisted, Thomas
APPLICANT: Kjaerulf, Soren
APPLICANT: Andersen, Carsten
APPLICANT: Fuglsang, Claus Crone
TITLE OF INVENTION: Alpha-amylase mutants with altered properties
FILE REFERENCE: 10062.200-US
CURRENT APPLICATION NUMBER: US/09/918, 543
CURRENT FILING DATE: 2001-07-31
NUMBER OF SEQ ID NOS: 30
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1
LENGTH: 1455
TYPE: DNA
ORGANISM: Bacillus sp.
FEATURE:
NAME/KEY: CDS
LOCATION: (1) ..(1455)
OTHER INFORMATION:
US-09-918-543-1

Query Match 65.7%; Score 1167; DB 9; Length 1455;
Best Local Similarity 87.6%; Pred. No. 4e-302;
Matches 1275; Conservative 0; Mismatches 180; Indels 0; Gaps 0;

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QY 238 CATCATATGGAAGGATGGAACCATGATGCAATTTTGAATGGCATTTGGCCAAATGAC 297
DB 1 CATCATATGGAACCAATGATGATGATGCAATTTTGAATGGATTTTGGCAATGAC 60
QY 298 GGAACCACTGGAACAGGTTACGAGATGACGAGCTTAATTAAAGATTAAGGATTAAC 357

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Db 61 GGGATCATTGGAACAGGTTGAGGATGACGAGCTAATTAAAGTAAGGATTAAC 120
QY 358 GCTGTTGATTCCTCTGATGGAAGGGAATTCGCAAAATGATGTTGGGTATGCTCC 417
Db 121 GCTGATGATCCACCTGATGGAAGGGAATTCGCAAAATGATGTTGGGTATGCTCC 180
QY 418 TATGATTTGATGATGTTGATGTTAAACCAAAAGGGAACCGTCCGTAACAAATATGCG 477
Db 181 TATGATTTATATATCTTGAGAGTTTACCAAGAGGGAACCGTCCGTAACAAATATGGA 240
QY 478 ACAAGAGTCAGTTGCAAGGTGCGTACATCTTTGAAAAATACGGAATTCAGTTTAT 537
Db 241 ACACGACACAGCTTACAGGCTGCGGTGACCTTTTAAAAATACCGCAATTCAGTATAT 300
QY 538 GGGGATGTCGTGATGATCATTAAGGTGACGACGAGCAAGATGTTAAATGCGGTG 597
Db 301 GGTGATGTCGTATGATCATTAAGGTGAGCAGATGTTACGGAATTTGAAATGCGGTG 360
QY 598 GAAGTGAACCGAAGCAACCGAAACCAAGAAATATCAGGTATACCATTTGAAGCATGG 657
Db 361 GAAGTGAATGAGCAACCGAAACCAAGAAATATCAGGTATACCATTTGAAGCATGG 420
QY 658 ACAGAAATTTGATTCCTGGAAGAGAAATATCCATTTCAACTTTAATGCGCTGTAT 717
Db 421 ACAGAAATTTGATTCCTGGAAGAGAAATATCCATTTCAACTTTAATGCGCTGTAT 480
QY 718 CATTGTTGATGGAACAGATTTGGGATCAGTCACTGATGTTGAAACAAATATTAATTC 777
Db 481 CATTGTTGATGGAACAGATTTGGGATCAGTCACTGATGTTGAAACAAATATTAATTC 540
QY 778 AGAGGTACCGGAAGGATGGAAGGATGGAAGTATATAGAAACCGCACTATGATTTAC 837
Db 541 AGGGAACAGGACAGGCTGGAAGGATGGAAGTATATAGAAACCGCACTATGATTTAC 600
QY 838 CTATGATGATGACAGATTTGATGATGATCATCAGAAATATCAATGAACTTAAATTCG 897
Db 601 CTATGATGATGACAGATTTGATGATGATCATCAGAAATATCAATGAACTTAAATTCG 660
QY 898 GGAATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 957
Db 661 GGAATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 720
QY 958 ATTAATATACAGTATACAGATGATGATGATGATGATGATGATGATGATGATGATGAT 1017
Db 721 ATTAATATACAGTATACAGATGATGATGATGATGATGATGATGATGATGATGATGAT 780
QY 1018 ATGTTTGCAGTTCAGAAATTTGAAAAATGACCTTGCTGCAATTCGAAAACTATTAAT 1077
Db 781 ATGTTTGCAGTTCAGAAATTTGAAAAATGACCTTGCTGCAATTCGAAAACTATTAAT 840
QY 1078 AAAACAAGTTGGAATCACTCCGTTGATGATGATGATGATGATGATGATGATGATGAT 1137
Db 841 AAAACAAGTTGGAATCACTCCGTTGATGATGATGATGATGATGATGATGATGATGATGAT 900
QY 1138 TCTAATATGAGTGGGATTTTGTATGAGAAATATTTTAAATGCTTCGTAACAAAA 1197
Db 901 TCTAATATGAGTGGGATTTTGTATGAGAAATATTTTAAATGCTTCGTAACAAAA 960
QY 1198 CACCTATACATGACAGTCAATTTGTTGATATACCATGACTCTGACGAGAGAGATTTG 1257
Db 961 CACCTATACATGACAGTCAATTTGTTGATATACCATGACTCTGACGAGAGAGATTTG 1020
QY 1258 GAATCTTTTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1317
Db 1021 GAATCTTTTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1080
QY 1318 CAAGTTTACCTTCGATTTTACGAGTATACAGGTATACCACTGATGATGATGATGATG 1377
Db 1081 CAAGTTTATCTTCGATTTTATGAGGATATACAGGTATACCACTGATGATGATGATG 1140
QY 1378 TCGATGAATCTAATATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1437
Db 1141 GGTATGAATCTAATATGAGGATGATGATGATGATGATGATGATGATGATGATGATGAT 1200

QY 1438 CAACATGATTTATTTGATCATGATATTTATGCTGAGACGAGAGAGAGGAGCAGCTCC 1497
Db 1201 CAGCATGATTTATCTTATATCATGATGATGATGATGATGATGATGATGATGATGATGAT 1260
QY 1498 CACCAAAATTCAGAGCTTCCAACTATTTATGCTGATGAGGACGAGGGGTATTAATGATG 1557
Db 1261 CATCAAAATTCAGAGCTTCCAACTATTTATGCTGATGAGGATGATGATGATGATGATG 1320
QY 1558 TATGTCGGAAACATTAAGCTGCGCAAGTATGAGAGATATCACCGGAAATAGCTGTG 1617
Db 1321 TATGTCGGGAAAAATTAACCGGGAACAGTTTGGAGATATTAACCGGAAATAGGACAG 1380
QY 1618 ACCGTACCAATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1677
Db 1381 ACCGTACCAATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1440
QY 1678 GTTGGGTGAAGCAA 1692
Db 1441 GTTGGGTGAAGCAA 1455

RESULT 12
US-09-925-576C-1
; Sequence 1, Application US/09925576C
; Publication No. US20030129718A1
; GENERAL INFORMATION:
; APPLICANT: Andersen, Carsten
; APPLICANT: Borcherdt, Torben Vedel
; APPLICANT: Nielsen, Bjarne Ronfeldt
; TITLE OF INVENTION: Amylase Variants
; FILE REFERENCE: 10004.204-US
; CURRENT APPLICATION NUMBER: US/09/925,576C
; NUMBER OF SEQ ID NOS: 20
; FILING DATE: 2001-08-09
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 1455
; TYPE: DNA
; ORGANISM: Bacillus sp.
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1455)
; OTHER INFORMATION: SP690
US-09-925-576C-1

Query Match 65.7%; Score 1167; DB 10; Length 1455;
Best Local Similarity 87.6%; Pred. No. 4e-302;
Matches 1275; Conservative 0; Mismatches 180; Indels 0; Gaps 0;
QY 238 CATCATATGAGGACGAATGGGACCATGATGATGATGATGATGATGATGATGATGATGATG 297
Db 1 CATCATATGAGGACGAATGGGACCATGATGATGATGATGATGATGATGATGATGATGATG 60
QY 298 GGGAACTATGGAACAGTTTACAGATGACGACGATTAACCTTAAAGATTAAGGATTAAC 357
Db 61 GGGAACTATGGAACAGTTTACAGATGACGACGATTAACCTTAAAGATTAAGGATTAAC 120
QY 61 GGGAACTATGGAACAGTTTACAGATGACGACGATTAACCTTAAAGATTAAGGATTAAC 120
Db 358 GCTGTTGATTCCTCTGATGGAAGGGAACCTTGCAAAATGATGTTGGGTATGCTCC 417
QY 121 GCTGTTGATTCCTCTGATGGAAGGGAACCTTGCAAAATGATGTTGGGTATGCTCC 180
QY 418 TATGATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 477
Db 181 TATGATTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 240
QY 478 ACAAGAGTCAGTTGCAAGGTGCGTACATCTTTGAAAAATACGGAATTCAGTTTAT 537
Db 241 ACACGACACAGCTTACAGGCTGCGGTGACCTTTTAAAAATACCGCAATTCAGTATAT 300
QY 538 GGGGATGTCGTGATGATCATTAAGGTGACGACGAGCAAGATGTTAAATGCGGTG 597
Db 301 GGTGATGTCGTATGATCATTAAGGTGAGCAGATGTTACGGAATTTGAAATGCGGTG 360

QY	598	GAAGTGAACCCGAAGCAACCGAATCAAGAAATATACAGAGTAADACCACTTGAAGATGG	657
Db	361	GAAGTGAATCGAGACACCGAACCAGAAACCTCAGGAGAGTATGCAATTAAGCGCTGG	420
QY	658	ACGAATTTGATTTCCCTGGAGAGAGAAATACCATTCCAACTTTAAATAGCGCTGTAT	717
Db	421	ACAAAGTTGATTTTCTGTGAAGAGGAATTAACATTCAGCTTTAAGTGGCGCTGTAT	480
QY	718	CATTTTGATGGGACGATTTGGGATCAGTACGCTCAGCTTCAGAACAAATATATAATTC	777
Db	481	CATTTTGATGGGACGATTTGGGATCAGTACCGCCAGCTTCAAAACAAATATATAATTC	540
QY	778	AGAGGTACCGGAAAGGCATGGGACCTGGGAAAGTAAATATAGAAACCGCAACTATAC	837
Db	541	AGGGAAACAGGCAAGGCGCTGGGACCTGGGAAAGTCAGTACGAAGAAATGGCAACTAT	600
QY	838	CTTATGTATGACGACATTTGATATGATCATCCAGAAATATCAATGAACCTTAGAAATGG	897
Db	601	CTTATGTATGACGACATTTGATATGATCATCCAGAAATATCAATGAACCTTAGAAATGG	660
QY	898	GGAGTTTGGTATACAAATACACTTAATCTAATGGAATTTGAATCGATGCTGTAAACAT	957
Db	661	GGAGTGTGGTATACAAATACACTTAATCTAATGGAATTTGAATGATGATGCAATGAAACAT	720
QY	958	ATTAATATACAGTATATCCAGAGATTTGGCTTAACAATGTGCTTAACACACAGCTTAACCA	1011
Db	721	ATTAATATATAGCTTTATACGAGATTTGGCTTTACATATGTGCTTAACACACAGCTTAACCA	780
QY	1018	ATGTTTGACGTGACGAATTTTGGAAAAATGACCTTGGCGCAATGGAAACATATTTAAT	1077
Db	781	ATGTTTGACGTGACGTGATTTTGGAAAAATGACCTTGGCGCAATGGAACATATTTGAAT	840
QY	1078	AAAACAGATGGAAATCACTCCGTGTCGATGTCTCTTCATTATTAATTTTGACATGCA	1137
Db	841	AAAACAGATGGAAATCACTCCGTGTTGATGTCTCTTCATTATTAATTTTGACATGCA	900
QY	1138	TCTAATAGTGGGCTATTTTGATATAGAAATATTTTAATGTTCTGTGCTACAAAA	1197
Db	901	TCTAATACGGGTGTTATATGATATAGAAATATTTTAATGTTCTGTGCTGCAAAAA	960
QY	1198	CACCTATACATNGACGACANTTTGTGATACCATGACTCCACCGAGAAACCATTTG	1257
Db	961	CATCCAAACAGTCCGTTACTTTGTGTATTAACATGATCTCCACCCGGGGAAACATTG	1020
QY	1258	GAATCCTTTGTTCAATCGTNGGTTCAACACACGAGGATATGCAATGATCTGCAAGGGAG	1317
Db	1021	GAATCCTTTGTTCAACATGTTTAAACACTTGCAATATGCAATGTGTTGCAAGGGAA	1080
QY	1318	CAAGTTAACCTTCGGTATTTTACGGGTATTAATAACGATTAACAATCATNGTGTCT	1377
Db	1081	CAAGGTATTCCTTCGGTATTTTATAGGGGATTAATAACGATTAACAATCATNGTGTCT	1140
QY	1378	TCGATGAATCTTAAATTTGATTCATCTTCTGACGAGCACTCAAGGATATGCTTAGGAAAC	1437
Db	1141	GCTATGAATCTTAAATTTGATTCATCTTCTGACGAGCACTCAAGGATATGCTTAGGAAAC	1200
QY	1438	CAACATGATTAATTTGATCATCATGATATTAATCCGCTGGAACGAGAGAAAGGGGACAGCTCC	1497
Db	1201	CAGCATGATTAATTTGATCATCATGATATTAATCCGCTGGAACGAGAGAGGAAATATGCTCC	1260
QY	1498	CACCCAAATTCAGGACTTGCACATTAATATGTCGATGGGCCAGGGGGTATTAATATGATG	1557
Db	1261	CATCCAAATTCAGGGCTTGGCCACCATTAATATGTCAGATGGTCCAGGTGGTAAACAATATGATG	1320
QY	1558	TATGTGCGGAAAACATTAAGCTGGCCAAATATGAGAGATATCACCGGAAATATGCTGTGCT	1617
Db	1321	TATGTGCGGAAAACATTAAGCTGGGCAAAATTTGAGAGATATTAATCCGGAATATGCAAGAGC	1380
QY	1618	ACCGTCAACATTAATAGGATGTTGGGGGAAATTTCACTGTAAACGAGGGGCAAGCTTTCG	1677
Db	1381	ACCGTCAACATTAATAGGATGAGATGGGGTATATTTCTCTGTAAATAGAGGGTCCGTTTTCG	1440

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OY      1678 GTTGGGTGAAGCAA 1692
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Db      1441 GTTGGGTGAAGCAA 1455

RESULT 13
US-10-025-648-4
; Sequence 4, Application US/10025648
; Publication No. US20030064908A1
; GENERAL INFORMATION:
;   APPLICANT: Bisgard-Frantzen, Henrik
;             Svendsen, Allan
;             Borchert, Torben Vedel
; TITLE OF INVENTION: AMYLASE VARIANTS
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Novo Nordisk of North America, Inc.
;   STREET: 405 Lexington Avenue, Suite 6400
;   CITY: New York
;   STATE: New York
;   COUNTRY: U.S.A.
;   ZIP: 10174-6401
; COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/10/025,648
;   FILING DATE: 19-Dec-2001
;   CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: 08/600,656
;   FILING DATE: 13-FEB-1996
; ATTORNEY/AGENT INFORMATION:
;   NAME: Lambiris, Elias J.
;   REGISTRATION NUMBER: 33,728
;   REFERENCE/DOCKET NUMBER: 4318.204-US
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 212 867 0123
;   TELEFAX: 212 867 0298
; INFORMATION FOR SEQ ID NO: 4:
;   LENGTH: 1455 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;   MOLECULE TYPE: DNA (genomic)
;   SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-025-648-4

Query Match      65.7%; Score 1167; DB 14; Length 1455;
Best Local Similarity 87.6%; Pred. No. 4e-302;
Matches 1275; Conservative 0; Mismatches 180; Indels 0; Gaps 0

OY      238 CATCATATATGGAGCAATGGAGCACCATGATGACGATATTTTGAATGCGCATTTGCCAAATGAC 297
      |||||
Db      1 CATCATATATGGAAACAATGGATGATATGATGATGCAATATTTTGGATGCTATTTGCCAAATGAC 60

OY      298 GGGAAACACTGGAAACAGTTTACGAGATGACGACGACTTAACCTTAAGAGTTAAAGGCAATTAC 357
      |||||
Db      61 GGGAAATCATTTGGAAACAGTTTGAAGGATGACGACGACTTAACCTTTAAAGATTAAGGCAATTACA 120

OY      358 GCTGTTTGGATTCCTCCGTCATGGAAGGGGACTTCGCAAAATGATGTTGGGATATGATGCC 417
      |||||
Db      121 GCTTATATGATCCCACTTCGTCATGGAAGGGGACTTCGCAAGATGATGTAAGTTATGAGACC 180

OY      418 TATGATTTGATACATCTTGTGTGACTTTTAAACCAAAAGGAAACCGTCGATACAAATATGAC 477
      |||||
Db      181 TATGATTTATATATGATCTTTGGAGAGATTTTAAACGAAGGGGACGTTTCGTAACAAATATGAGA 240

OY      478 ACAAGAGTCAGTTTGCAGAGTGCCTGTACATCTTTGAAAAATTAACGGGATTCGAAGTTAT 537
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Db 241 ACACGACACGAGTACAGCTGGGCTGACCTCTTTAAAAATAACGGCATTGAGTATAT 300
Qy 538 GGGGATGTCGTGATGATCTATAAGGTGAGCAGACGGGACAGATGCTAAATGGGGTG 597
Db 301 GGTGATGTCGTGATGATCTATAAGGTGAGCAGATGCTAAATGGGGTG 360
Qy 598 GAAGTGAACCGAAGCAGACCGAAACCAAGAAATATCAGGTATATCACATGAAGCATGG 657
Db 361 GAAGTGAATCGAGACACCGAAACCAAGAAATATCAGGTATATCACATGAAGCATGG 420
Qy 658 ACGAAATTTGATTTCCCTGGAGAGGAAATATCCATTCATCTTAATATGCGCTGGTAT 717
Db 421 ACGAAATTTGATTTCCCTGGAGAGGAAATATCCATTCATCTTAATATGCGCTGGTAT 480
Qy 718 CATTTGATGGAGACAGATTGGGATCAGTCACTGACGTTGAGAACAAATATATTAATTC 777
Db 481 CATTTGATGGAGACAGATTGGGATCAGTCACTGACGTTGAGAACAAATATATTAATTC 540
Qy 778 AGAGGTACCGGAAAGGATGGGACCTGGGAGTAGATATAGAGAACGGGACATATGATTAC 837
Db 541 AGGGGAAACAGGACAGGCTGGGAGCTGGGAGTAGATATAGAGAAATGGGAACTATGACTAT 600
Qy 838 CTATGATGACAGACATTTGATGATCATCCAGAGTAATCAATGAATTAAGAAATTTGG 897
Db 601 CTATGATGACAGACATTTGATGATCATCCAGAGTAATCAATGAATTAAGAAATTTGG 660
Qy 898 GGAAGTTGGTATACAAATACACTTAATCTAGATGATTTAGAAATCGATGCTGGAAACAT 957
Db 661 GGAAGTTGGTATACAAATACACTTAATCTAGATGATTTAGAAATAGATGACATGAAACAT 720
Qy 958 AATTAATACAGCTATACAGAGATGGGCTAACACATGGGTAACACACAGGTAACCA 1017
Db 721 AATTAATACAGCTATACAGAGATGGGCTAACACATGGGTAACACACAGGTAACCA 780
Qy 1018 ATGTTTCAGTTCGAGAAATTTTGGAAAAATGACCTTGCTCAATCGAAAACTAATTTAAT 1077
Db 781 ATGTTTCAGTTCGAGAAATTTTGGAAAAATGACCTTGCTCAATCGAAAACTAATTTAAT 840
Qy 1078 AAAACAAGTTGGAATCACTCCGCTGTCGATGTTCTCTTCAATTAATTTGTAACATGCA 1137
Db 841 AAAACAAGTTGGAATCACTCCGCTGTCGATGTTCTCTTCAATTAATTTGTAACATGCA 900
Qy 1138 TCTAATGCTGGTCTATTTTGTATGATGAGAAATTTTAAATGGTCTGTCGTAACAAAA 1197
Db 901 TCTAATGCTGGTCTATTTTGTATGATGAGAAATTTTAAATGGTCTGTCGTCANAAAA 960
Qy 1198 CACCTATACATGACATGACATTTGTTGATTAACCATGACTCTGACCGAGAGAACATTTG 1257
Db 961 CATCAACACATGCGCTTACTTTTGTGATTAACCATGACTCTGACCGAGAGAACATTTG 1020
Qy 1258 GAATCTTTTGTTCATGCTGCTGTCACAAACCACTGGCATAATGATTTGTAACAGGAG 1317
Db 1021 GAATCTTTTGTTCATGCTGCTGTCACAAACCACTGGCATAATGATTTGTAACAGGAG 1080
Qy 1318 CAAGGTACCTTCCGATTTTAAAGGTGATTAACGATTAACCAATCAATGAGTTCCT 1377
Db 1081 CAAGGTATCTCTCCGATTTTAAAGGTGATTAACGATTAACCAATCAATGAGTTCCT 1140
Qy 1378 TCGATGAATCTAAATTTGATCTGCTCTGACAGGACGTCMAAGTATGCTACGAAACC 1437
Db 1141 GCTATGAATCTAAATTTGATCTGCTCTGACAGGACGTCMAAGTATGCTATGCTAACG 1200
Qy 1438 CAACATGATTAATTTTGTATCATGATATTAATGCGCTGGACGAGAGAAAGGACAGCTCC 1497
Db 1201 CAGATGATTAATTTTGTATCATGATATTAATGCGCTGGACGAGAGAAAGGAAATAGCTCC 1260
Qy 1498 CACCAATTTACAGACATTTGACAACTATTAATGTCGATGGGACAGGAGGTAATTAATG 1557
Db 1261 CATCAAAATTTACAGGCTTTGACCAATTAATGTCGATGGGACAGGAGGTAATTAATG 1320
Qy 1558 TATGTGGGAAAACTAATAGCTGGCCAAATGATGAGAGATATCAACGGAAATAGGCTGCT 1617
Db 1321 TATGTGGGAAAACTAATAGGCGGACAAATTTGGAGAGATATTAACGGAAATAGGACAGGC 1380
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Qy 1618 ACCGTACCATTAATGACAGATGTTGGGGAAATTTCACTGTAAACGAGGGGACAGTTGG 1677
Db 1381 ACCGTACCATTAATGACAGATGTTGGGGAAATTTCTCTGTATATGAGAGGCTCGTTGG 1440
Qy 1678 GTTTGGGTGAAGCAA 1692
Db 1441 GTTTGGGTGAAGCAA 1455

RESULT 14
US-10-327-837-9
; Sequence 9, Application US/10327837
; Publication No. US20030211958A1
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Borchert, Torben Vedel
; APPLICANT: Bisgaard-Frantzen Henrik
; APPLICANT: Ouetrup, Helle
; APPLICANT: Nielsen, Bjarne Ronfeldt
; APPLICANT: Nielsen, Vibeke Skovgaard
; APPLICANT: Hoeck, Lisbeth Hedegaard
; TITLE OF INVENTION: Novel -Amylase And -Amylase Mutants
; FILE REFERENCE: 5276.400-US
; CURRENT APPLICATION NUMBER: US/10/327,837
; PRIOR FILING DATE: 1999-04-13
; PRIOR APPLICATION NUMBER: US/09/290,734
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 9
; LENGTH: 1455
; TYPE: DNA
; ORGANISM: Bacillus sp.
US-10-327-837-9

Query Match 65.7%; Score 1167; DB 17; Length 1455;
Best Local Similarity 87.6%; Pred. No. 4e-302;
Matches 1275; Conservative 0; Mismatches 180; Indels 0; Gaps 0;

Qy 238 CATCATTAATGAGCAGATGGGACCATGATGACATATTTTGAATGGCATTTGCCAAATGAC 297
Db 1 CATCATTAATGAGCAGATGGGACCATGATGACATATTTTGAATGGCATTTGCCAAATGAC 60
Qy 298 GGGAAACCATGGAACAGGTTTACGAGATGACGACGTAACCTTAAGATGAAGGATTAAC 357
Db 61 GGGAAATCATTTGAACAGGTTTACGAGATGACGACGTTAATTAAGATGAAGGATTAACA 120
Qy 358 GCTGTTGATTTCTCTCTGATGAGAGGGGACCTTCCAAATGATGTTGGTATGGTCC 417
Db 121 GCTGTTGATTTCTCTCTGATGAGAGGGGACCTTCCAAATGATGTTGGTATGGAGCC 180
Qy 418 TATGATTTGATGATTTGTTGATGATTTTAAACCAAAAGGAAACCTCGGTACAAATATG 477
Db 181 TATGATTTTATGATCTTTGAGAGGTTTAAACCAAAAGGAGCGGTTGTACAAATATGGA 240
Qy 478 ACAAGAGTATGTTGCAAGGTGCGCTGACATCTTTGAAAAATAACGGGATTCAGTTTAT 537
Db 241 ACAAGAGTATGTTGCAAGGTGCGGTGACCTTTTAAAAATAACGGGATTCAGTTTAT 300
Qy 538 GGGGATGTCGTGATGATCTATAAGGTGAGCAGACGGGACAGAGATGTAATGGCGTG 597
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Qy 598 GAAGTGAACCGAAGCAGACCGAAACCAAGAAATATCAGGTATATCACATGAAGCATGG 657
Db 361 GAAGTGAATCGAGACACCGAAACCAAGAAATATCAGGTATATCACATGAAGCATGG 420
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Qy 838 CTTATGATGAGACATGATATGATATCATCAGAAATATCAATGAATGAATGG 897
Db 601 CTTATGATGAGACATGATATGATATCATCAGAAATATCAATGAATGAATGG 660
Qy 898 GGAGTTGGTATACAAATATACCTTAATCTAGATGATATGATATGATGATGAT 957
Db 661 GGAGTTGGTATACAAATATACCTTAATCTAGATGATATGATATGATGATGAT 720
Qy 958 ATTAAATACAGCTATACAGAGATGGCTTAACATGTCGCTAACACCAAGTAA 1017
Db 721 ATAAATATATACCTTATACAGAGATGGCTTAACATGTCGCTTAACACCAAG 780
Qy 1018 ATGTTGAGTTGAGATTTTGGAAATAGACCTTGCTGCAATGCAAACTATTTA 1077
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Qy 1258 GAATCCTTTGTTCAATCGTGGTCAAAACACCTGCAATGATGATCTGCAAG 1317
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Qy 1618 ACCGTACCATTAATGAGATGTTGGGGAATTTCACTGTAACGAGGAGGAG 1677
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RESULT 15
 US-10-327-837-14
 ; Sequence 14, Application US/10327837
 ; Publication No. US20030211958A1
 ; GENERAL INFORMATION:

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; APPLICANT: Svendsen, Allan
; APPLICANT: Borchert, Torben Vedel
; APPLICANT: Bisgard-Frantzen Henrik
; APPLICANT: Outtrup, Helle
; APPLICANT: Nielsen, Bjarne Romfeldt
; APPLICANT: Nielsen, Vibeke Skovgaard
; APPLICANT: Hoeck, Lisbeth Hedegaard
; TITLE OF INVENTION: Novel -Amylase And -Amylase Mutants
; FILE REFERENCE: 5276,400-US
; CURRENT APPLICATION NUMBER: US/10/327,837
; PRIOR FILING DATE: 2002-12-23
; PRIOR APPLICATION NUMBER: US/09/290,734
; NUMBER OF SEQ. ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 14
; LENGTH: 1455
; TYPE: DNA
; ORGANISM: Bacillus sp.
; US-10-327-837-14

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Query Match 65.7%; Score 1167; DB 17; Length 1455;
 Best Local Similarity 87.6%; Pred. No. 4e-302;
 Matches 1275; Conservative 0; Mismatches 180; Indels 0; Gaps 0;

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Qy 238 CATCATATGAGAGAGATGGGACCATGATGACATTTTGAATGGCAATTTGCCAAATGAC 297
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Qy 358 GCTGTTGATCTCTCTGCAATGAGGAGCTTGCAGAAATGATGTTGGTATGTC 417
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Db 301 GGGGATGCTGATGATTAATTAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 360
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Db 481 CATTTGATGAGACAGATTTGGATCACTACGCTCACTTCAAGCAAAATATATTAATTC 540
Qy 778 AGAGTACCGGAAAGGAGTGGAGTGGAGATGATATTAAGAAAGGCACTATGATAC 837
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: May 2, 2005, 17:25:37 ; Search time 4003 Seconds
(without alignments)
16887.870 Million cell updates/sec

Title: US-08-952-741-1
Perfect score: 1776
Sequence: 1 atataaattgaaatgacac.....ccaatacaattggaagctc 1776

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

EST: *
1: gb_esc1: *
2: gb_esc2: *
3: gb_esc3: *
4: gb_esc4: *
5: gb_esc5: *
6: gb_esc6: *
7: gb_esc7: *
8: gb_esc8: *
9: gb_esc9: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	168.2	9.5	784	7	CF699180 CCAHS23TR
2	168.2	9.5	795	7	CF684098 CCAAG203TR
3	168.2	9.5	796	7	CF684188 CCAEQ87TR
4	168.2	9.5	861	7	CF712259 CCAQY84TR
5	168.2	9.5	877	7	CF687730 CCAQY84TR
6	168.2	9.5	888	7	CF675857 CCAQY84TR
7	168.2	9.5	889	7	CF685247 CCAQY84TR
8	163.2	9.2	773	7	CF684810 CCAQY84TR
9	163.2	9.2	798	7	CF697851 CCAQY84TR
10	162.6	9.2	793	7	CF700043 CCAQY84TR
11	160.6	9.0	752	7	CF708585 CCAQY84TR
12	141.8	8.0	727	7	CF717666 CCAQY84TR
13	136.8	7.7	741	7	CF705868 CCAQY84TR
14	126.2	7.1	856	8	CC131534 CCAQY84TR
15	124.6	7.0	876	8	BH377207 AG-ND-109
16	103.8	5.8	534	8	BH379485 AG-ND-124
17	97.6	5.5	885	7	CF685239 CCAQY84TR
18	96.8	5.5	652	7	CF643218 D61_C12 F
19	96.8	5.5	689	7	CF642012 D46_G07 F
20	95.4	5.4	685	6	CD488238 T06_D07 T
21	90.8	5.1	428	5	BH639413 mgcw013xN
22	89.4	5.0	426	7	CF642668 D54_E06 F
23	87.4	4.9	741	7	CF699170 CCAHS23TR
24	87.4	4.9	784	7	CF697840 CCAQY84TR

C 25	87.4	4.9	804	7	CF685993 CCAAB1TF
C 26	87.4	4.9	825	7	CF684087 CCAQY84TR
C 27	87.4	4.9	838	7	CF675850 CCAQY84TR
C 28	87.4	4.9	841	7	CF717658 CCAQY84TR
C 29	87.4	4.9	847	7	CF708576 CCAQY84TR
C 30	87.4	4.9	852	7	CF684179 CCAQY84TR
C 31	87.4	4.9	897	7	CF684804 CCAQY84TR
C 32	87.4	4.9	895	7	CF712253 CCAQY84TR
C 33	87.4	4.9	918	7	CF687718 CCAQY84TR
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C 35	82.8	4.7	491	7	CO138160 EST832831
C 36	82.8	4.7	530	7	CO148623 EST832836
C 37	82.8	4.7	535	7	CO138237 EST832908
C 38	82.2	4.6	1628	8	BZ424843 100020232
C 39	79.8	4.5	394	5	BU640392 mgcw019XO
C 40	77.2	4.3	532	1	AU188400 AU188400
C 41	77.2	4.3	1407	9	CU945603 OBI88005
C 42	76.2	4.3	494	7	CF700027 CCAQY84TR
C 43	71.8	4.0	289	6	CD271159 T143A0213
C 44	71.8	4.0	599	7	CO148015 EST823068
C 45	71.8	4.0	614	7	CF644164 K17_F07 F

ALIGNMENTS

RESULT 1
LOCUS CF699180 784 bp mRNA linear EST 16-AUG-2004
DEFINITION CCAHS23TR C.neoformans strain JEC21 Cryptococcus neoformans var. neoformans CDNA clone CCAHS23, mRNA sequence.
VERSION CF699180
KEYWORDS CF699180.1 GI:41553339
SOURCE EST.
ORGANISM Cryptococcus neoformans var. neoformans (Filobasidiella neoformans var. neoformans)
REFERENCE Cryptococcus neoformans var. neoformans
AUTHORS Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Filobasidiellales; Tremellaceae; Filobasidiella.
TITLE 1 (bases 1 to 784)
Loftus, B.
JEC21 cDNA library
Unpublished (2003)
COMMENT Other ESTs: CCAHS23TF
Contact: Brendan Loftus
TIGR
Department of Bacteriologic Genomics, TIGR, 9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-3543
Fax: 301-838-0208
Email: crypt@tigr.org
Seq primer: TR.
FEATURES
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/note="Vector: pCMVSPORT6; Site 1: NotI EcoRV; The full length, normalized library was prepared from a variety of conditions using RNA provided by Joseph Heitman and Jennifer Lodge"

ORIGIN
Query Match 9.5%; Score 168.2; DB 7; Length 784;
Best Local Similarity 53.5%; Pred. No. 2.2e-34;
Matches 375; Conservative 0; Mismatches 323; Indels 3; Gaps 1;
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Db      70 ACATATATGAGTACTTCAATGCTGACGCTGAAGTGTGTGTACATTTGAAAAAGTAT 129
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Qy      439 GAGTTTAACCAAAAGGAAACCGTCCGTACAATAATGSCAACAAGATCGATGCAAGT 498
Db      250 GAATTCGACCAAGAAAGATCTGTCTGATCAAAATGGGGTACTAAGAAGATCTTTAAAA 309
Qy      499 GCCGTGACATCTTTGAAAAATAACGGGATTCAAATTATGGGGATGTCGTGATGAATCAT 558
Db      310 GCATTTAAGGCTGCTTCTGGAAGGGCATTTATCACTGATGATGCTGTTGGAATCAC 369
Qy      559 AAGGTGAGACAGACGGGACAGAGATGTTAATGCGGTGGAAGTGAACGGAACCAACGA 618
Db      370 AAGGCGGCGCTGATGATTAAGAAATTTATGCGCACATGATGAGACGAATTAACCT 429
Qy      619 AACCAAGAAATATCAGGTGAATACACCATTTGAAGATGACGAATTTGATTTCCCTGCA 678
Db      430 AACAGGAATAGAGAAATGACAAATTTGAAGGCTGACCAAGTTCACTTTCCCTGGC 489
Qy      679 AAGGAATATCCATTTCACTTTAAATGCGCTGATATCTTTGATGGGAATGATGG 738
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Qy      799 GACTGGAAATAGATATAGAAACGGCACTATGATTAATCTTATGATGACATTTGAT 858
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Qy      859 ATGAGATCATCAGAAATTAATCAATGAATTAAGAAATTTGGAGTTGGTATCAAAATCA 918
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LOCUS      CCAAG203TR C.neoformans strain JEC21 Cryptococcus neoformans var.
DEFINITION      neoformans CDNA clone CCAAG203, mRNA sequence.
ACCESSION      CF684098
VERSION      CF684098.1
KEYWORDS      GI:41538257
SOURCE      EST.
ORGANISM      Cryptococcus neoformans var. neoformans (Filobasidiella neoformans
var. neoformans)
Crytoccoccus neoformans var. neoformans
Bukaryota; Fungi; Basidiomycota; Hymenomycetes;
Heterobasidiomycetes; Tremellomycetidae; Tremellales; Tremellaceae;
Filobasidiella.
1 (bases 1 to 795)
Loftus, B.
End sequencing of clones from a full length enriched, normalized
JEC21 cDNA library
Unpublished (2003)
Other ESTs: CCAAG203TF
Contact: Brendan Loftus
TIGR
Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,
Rockville, MD 20850, USA
Tel: 301-838-3543

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Location/Qualifiers
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length, normalized library was prepared from a variety of
conditions using RNA provided by Joseph Heitman and
Jennifer Lodge"

ORIGIN
Query Match      9.5%; Score 168.2; DB 7; Length 795;
Best Local Similarity 53.5%; Pred. No. 2,2e-34;
Matches 375; Conservative 0; Mismatches 323; Indels 3; Gaps 1;

Qy      259 ACCATATGACGATTTTAAATGCGATTTGCCAATGACGGGACACACTGGAACAGTTA 318
Db      83 ACATATGATCAGTACTTCAATGCTGACGCTGAAGGTGTGTGATATTGAAAAAGTAT 142
Qy      319 CGAGATGACGACCTTAATTAAAGATTAAAGGATTACCGCTGTTGGATTCTCTGCA 378
Db      143 GAAAGGATCCGAAAGACTGCGCAACATGGGATCACTGCTGTGGATTCTCTCTCT 202
Qy      379 TGGAGGGAATTCGCAAAATGATGTTGGTATGTCCTTATGATTTGTAAGATCTTGGT 438
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Qy      439 GAGTTTAACCAAAAGGAAACCGTCCGTACAATAATGSCAACAAGATCGATGCAAGT 498
Db      263 GAATTCGACCAAGAAAGATCTGTCTGATCAATGCGGTACTTAAGAAGATCTTTAAAA 322
Qy      499 GCGGTACATCTTTGAAAAATAACGGGATTCAAATTATGGGGATGTCGTGATGATCAT 558
Db      323 GCATTTAAGGCTCTTCTGGAAGGGCATTTACAGTATGATGATGCTGTTGAATCAC 382
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Db      383 AAGGCGGCGCTGATGATTAAGAAATTTATGCGCACCATGATGAGACGAATTAACCGT 442
Qy      619 AACCAAGAAATATCAGGTGAATTAACCATTTGAAGCAATGCAAAATTTGATTTCCCTGCA 678
Db      443 AACAGGAATAGAGAAATGCAACATTTGAAGGCTGACCAAGTTCACTTTCCCTGGC 502
Qy      679 AAGGAATATACCATTTCAACTTTAAATGCGCTGTGATCATTTTGTGATGGGACAGATTGG 738
Db      503 AAGGGGACAGATCTCCGACATGAAGTGAATTTTAACATTTTCAAGGGTGAAGCT-- 560
Qy      739 GATCAGTACGTCAGCTTCAGAACAAATATATTAATTCAGAGTACCGGAAGGATGG 798
Db      561 -ATGAGCGCAAGACTGAGACCAACCGCTATCTTCAATTCAGAGGGGACGGAAGCATTTGG 619
Qy      799 GACTGGAAATAGATATAGAAACGGCACTATGATTAATCTTATGATGACATTTGAT 858
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Qy      859 ATGAGATCATCAGAAATTAATCAATGAATTAAGAAATTTGGAGTTGGTATCAAAATCA 918
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RESULT 3
CF684188      796 bp      mRNA      linear      EST 16-AUG-2004
LOCUS
CF684188

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LOCUS								
DEFINITION								
CCACY84TR C.neoformans strain JEC21 Cryptococcus neoformans var.								
neoformans CDNA clone CCACY84, mRNA sequence.								
CF712259								
VERSION								
KEYWORDS								
SOURCE								
EST.								
CF712259.1								
GI:41566418								
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var. neoformans)								
Cryptococcus neoformans var. neoformans								
Eukaryota; Fungi; Basidiomycota; Hymenomycetes;								
Heterobasidiomycetes; Tremellomycetidae; Tremellales; Tremellaceae;								
Filobasidiella.								
1 (bases 1 to 861)								
Loftus B.								
End sequencing of clones from a Full length enriched, normalized								
JEC21 cDNA library								
Unpublished (2003)								
Other ESTs: CCACY84TO								
Contact: Brendan Loftus								
TIGR								
Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,								
Rockville, MD 20850, USA								
Tel: 301-838-3543								
Fax: 301-838-0208								
Email: crypt@tigr.org								
Seq primer: TR.								
Location/Qualifiers								
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conditions using RNA provided by Joseph Heltman and								
Jennifer Lodge"								
ORIGIN								
Query Match								
Best Local Similarity								
Matches								
375;								
Conservative								
0;								
Mismatches								
333;								
Indels								
3;								
Gaps								
1;								
259								
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CGGGAAC								
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 DB 299 GCATTTAAGGCTCTTCTGTGAAGAGGCATTATACGTAATGATGCTTTGAATCAC 358
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 QY 619 AACCAAGAAATATCAGGTGATATCACCATTGAAGCATGACGAATTTGATTTCCCTGGA 678
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 QY 679 AGAGAAATACCATTCACATTTAAATGCGCGGTGATTTGATTTGAGGACAGATTGG 728
 DB 479 AGAGGCGACAGATCTCCACATGAAATGTAATTTAACATTTTCACAGGGGTAAGT-- 536
 QY 739 GATCAGTCAGTCAGCTTCAGAACAAATATATTAATTCAGAGGTACCGGAAGGATGG 798
 DB 537 -ATGACGCAAAAGACTGAGACACCGCTATCTTCAAGGATTCAGGGGAGCAATGG 595
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RESULT 8 773 bp mRNA linear EST 16-AUG-2004
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 LOCUS CCADG907R C.neoformans strain JEC21 Cryptococcus neoformans var.
 DEFINITION neoformans cDNA clone CCADG90, mRNA sequence.

ACCESSION CF684810
 VERSION CF684810.1 GI:41538969
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 SOURCE Cryptococcus neoformans var. neoformans (Filobasidiella neoformans
 var. neoformans)
 ORGANISM Cryptococcus neoformans var. neoformans
 Eukaryota; Fungi; Basidiomycota; Hymenomycetes;
 Heterobasidiomycetes; Tremellomycetidae; Tremellales; Tremellaceae;
 Filobasidiella.
 1 (bases 1 to 773)

Loftus, B.
 TITLE End sequencing of clones from a Full length enriched, normalized
 JEC21 cDNA library
 JOURNAL Unpublished (2003)
 COMMENT Other ESTs: CCADG907F
 CONTACT: Brendan Loftus
 TIGR
 Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,
 Rockville, MD 20850, USA
 Tel: 301-838-3543
 Fax: 301-838-0208
 Email: crypt@tigr.org
 Seg primer: TR.

FEATURES
 source
 Location/Qualifiers
 1..773
 /organism="Cryptococcus neoformans var. neoformans"
 /mol_type="mRNA"
 /strain="JEC21"
 /db_xref="taxon:40410"
 /clone_1lb="C.neoformans strain JEC21"
 /note="Vector: pCMVSPORT6; Site_1: NotI EcoRV; The full
 length, normalized library was prepared from a variety of
 conditions using RNA provided by Joseph Heitman and

ORIGIN
 Jennifer Lodge"

Query Match 9.2%; Score 163.2; DB 7; Length 773;
 Best Local Similarity 54.3%; Pred. No. 5e-33;
 Matches 352; Conservative 0; Mismatches 293; Indels 3; Gaps 1;

QY 259 ACCATGATCAGATTTTGAATGCGATTTGCCAAATGAGGGGAACCATGGAACAGTTA 318
 DB 107 ACATATATCAGTACTTCCAAATGTAACGCTGAAGGTGATGATGATTTGAAAAAGTAT 166
 QY 319 CGAGATGACGACGCTAATTAAGATTAAGGATTAACCGTGTGATTTCTCTGCA 378
 DB 167 GAAGGAAATCCGAAGATCGGCAACATGGGATCATGCTGTGATTTCTCTCTCT 226
 QY 379 TGAAGGGAATCTCGAAATGATGTTGGGTATGTCCTATGATTTGACATCTTGGT 438
 DB 227 ACTAAGGCTTACCCCTAAGGATACAGATATGATTTATGATTTGGGACTTGGGA 286
 QY 439 GAGTTTAACCAAAAGGGAACCGTCCGTACAAATATGACACAGAGTCAGTTGCAAGT 498
 DB 287 GAATTTGACCAAGAAAGATCTGTGCTTACCAATGAGGATCTTAAGAAATCTTTAAA 346
 QY 499 GCCGTGACATCTTTGAAAAATAACGGGATTCAGATTATGGGATGCTGATGAATCAT 558
 DB 347 GCATTTAAGGCTGCTTCTGAGAAAGGCAATTATCAAGTATGATGATGCTGTTGAATCAC 406
 QY 559 AAGGTGAGACAGCGGACAGAGATGTAATGCGGTGAAAGTGAACCGAACACGA 618
 DB 407 AAGGCCGGCGGTGATATTAAGAAATTAATGAGCCACATGATGAGCAAGATTAACCGT 466
 QY 619 AACCAAGAAATATCAGGTGATATACCATTTGAAGCATGAGCAAAATTTGATTTCCCTGA 678
 DB 467 AACCAAGAAATGAGAAATGCAACATTTGAAGGTGAGCAAGTCACTTTCCCTGGC 526
 QY 679 AAGGAAATACCATTTCAACTTTAAATGCGCGTGTATCATTTTGTATGGAGCAGATTGG 738
 DB 527 AGAGGCGACAGATCTCCACATGAAATGGAATTTTAAACATTTTCACAGGGGATGACTAT 586
 QY 739 GATCAGTCAGTCAGCTTCAGAACAAATATATTAATTCAGAGGTACCGGAAGGATGG 798
 DB 587 GACGCAAGACTGAGACC--ACCGTATCTTCAAGATTCAGAGGAGCGGAAGCATGG 643
 QY 799 GACTGGGAATGATATGAGAACCGCACTATGATTAATGATGATGATGATGATGAT 858
 DB 644 GCCACCGATGTTATTAAGAAACCGGCTCTTCGATTTATCTCATGTTTCCGATATTGAC 703
 QY 859 ATGATCATCCAGAGATATCATGAACTTAGAAATTTGGGAGTTGG 906
 DB 704 CATTACACCCGATGTTGAGGCCGAACTCAACAAATGGGTAATGG 751

RESULT 9 798 bp mRNA linear EST 16-AUG-2004
 CF697851
 LOCUS CCAGQ427R C.neoformans strain JEC21 Cryptococcus neoformans var.
 DEFINITION neoformans cDNA clone CCAGQ42, mRNA sequence.

ACCESSION CF697851
 VERSION CF697851.1 GI:41552010
 KEYWORDS EST.
 SOURCE Cryptococcus neoformans var. neoformans (Filobasidiella neoformans
 var. neoformans)
 ORGANISM Cryptococcus neoformans var. neoformans
 Eukaryota; Fungi; Basidiomycota; Hymenomycetes;
 Heterobasidiomycetes; Tremellomycetidae; Tremellales; Tremellaceae;
 Filobasidiella.
 1 (bases 1 to 798)

REFERENCE JOURNAL
 AUTHORS Unpublished (2003)
 TITLE JEC21 cDNA library
 COMMENT Other ESTs: CCAGQ427F
 CONTACT: Brendan Loftus

TIGR
Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,
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Tel: 301-838-3543
Fax: 301-838-0208
Email: crypt@tigr.org
Seq primer: TR.

FEATURES
SOURCE

Location/Qualifiers
1..798
/organism="Cryptococcus neoformans var. neoformans"
/mol_type="rRNA"
/strain="JEC21"
/db_xref="taxon:40410"
/clone_lib="C.neoformans strain JEC21"
/note="Vector: pCMVSPORT6; Site 1: NotI EcoRV; The full
length, normalized library was prepared from a variety of
conditions using RNA provided by Joseph Heitman and
Jennifer Lodge"

ORIGIN

Query Match 9.2%; Score 163.2; DB 7; Length 798;
Best Local Similarity 54.3%; Pred. No. 5.1e-33;
Matches 352; Conservative 0; Mismatches 293; Indels 3; Gaps 1;

259 ACCATGATGCGATTTTGAATGCGATTTGCCAATGACGGAACTGGACAGCTTA 318
135 ACAATGATGCGATTTTGAATGCGATTTGCCAATGACGGAACTGGACAGCTTA 194
319 CGAGATGACGCGATTTTGAATGCGATTTGCCAATGACGGAACTGGACAGCTTA 378
195 GAAAGCGATTTTGAATGCGATTTGCCAATGACGGAACTGGACAGCTTA 254
379 TGAAGGCGATTTTGAATGCGATTTGCCAATGACGGAACTGGACAGCTTA 438
255 ACTAAGCGATTTTGAATGCGATTTGCCAATGACGGAACTGGACAGCTTA 314
439 GAGTTTAAACCAAAAGGAAAGCGATTTGCCAATGACGGAACTGGACAGCTTA 498
315 GAAATTCGACGAAAGATGCTGCGATTCGAAAGGAAAGCGATTTGCCAATGAC 374
499 GCGCGATTTTGAATGCGATTTGCCAATGACGGAACTGGACAGCTTA 558
375 GCATTAAGCGATTTTGAATGCGATTTGCCAATGACGGAACTGGACAGCTTA 434
559 AAAGTGAAGCAAGCGGACAGATGTAATGCGATTTGCCAATGACGGAACTGG 618
435 AAGCGCGATTTTGAATGCGATTTGCCAATGACGGAACTGGACAGCTTA 494
619 AACCAAGAAATATGAGGATTAACCGATTTGCCAATGACGGAACTGGACAGCT 678
495 AACCAAGAAATATGAGGATTAACCGATTTGCCAATGACGGAACTGGACAGCT 554
679 AGAGAAATATGAGGATTAACCGATTTGCCAATGACGGAACTGGACAGCTTA 738
555 AGAGGCGACAGTACTCGACATGAGTGAATTTTCACTTTACAGGGGTACATAT 614
739 GATCAGTCACTGACCTTCAAGACAAATATATTAATTCAGAGTACCGAAGGATG 798
615 GAGCAAGAGTGAAGC--ACCGTATCTTCAAGATTTCAAGGGGAGGAGATTTGG 671
799 GACTGGAGATGATATATGAGAGCGCACTATGATTTCTTATGATGACAGATGAT 858
672 GCCACCAATGTTGATTAAGAAAGCGGCTTTGATATTCATGTTTGGCGATATGAC 731
859 ATGATCATCCAGAGTAAATCAATGAATTTGAATGGGAGTTTGG 906
732 CATTCACACCGGATTTGAGCGCGAATCTCAACAAATGGGTAATGG 779

RESULT 10
CF700043
LOCUS CF700043 793 bp mRNA linear EST 16-AUG-2004

DEFINITION CCADY677R.C.neoformans strain JEC21 Cryptococcus neoformans var.
neoformans cDNA clone CCADY67, mRNA sequence.

ACCESSION CF700043
VERSION CF700043.1 GI:41554202

KEYWORDS

SOURCE

ORGANISM

Cryptococcus neoformans var. neoformans (Filobasidiella neoformans
var. neoformans)
Cryptococcus neoformans var. neoformans
Eukaryota; Fungi; Basidiomycota; Hymenomycetes;
Heterobasidiomycetes; Tremellomycetidae; Tremellales; Tremellaceae;
Filobasidiella.
1 (bases 1 to 793)
Lofthus, B.

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

End sequencing of clones from a Full length enriched, normalized
JEC21 cDNA library
Unpublished (2003)
Other ESTs: CCADY677F
Contact: Brendan Lofthus
TIGR
Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,
Rockville, MD 20850, USA
Tel: 301-838-3543
Fax: 301-838-0208
Email: crypt@tigr.org
Seq primer: TR.

FEATURES
SOURCE

Location/Qualifiers
1..793
/organism="Cryptococcus neoformans var. neoformans"
/mol_type="rRNA"
/strain="JEC21"
/db_xref="taxon:40410"
/clone_lib="CCADY67"
/note="Vector: pCMVSPORT6; Site 1: NotI EcoRV; The full
length, normalized library was prepared from a variety of
conditions using RNA provided by Joseph Heitman and
Jennifer Lodge"

ORIGIN

Query Match 9.2%; Score 162.6; DB 7; Length 793;
Best Local Similarity 54.4%; Pred. No. 7.4e-33;
Matches 349; Conservative 0; Mismatches 289; Indels 3; Gaps 1;

259 ACCATGATGCGATTTTGAATGCGATTTGCCAATGACGGAACTGGACAGCTTA 318
153 ACAATGATGCGATTTTGAATGCGATTTGCCAATGACGGAACTGGACAGCTTA 212
319 CGAGATGACGCGATTTTGAATGCGATTTGCCAATGACGGAACTGGACAGCTTA 378
213 GAAAGCGATTTTGAATGCGATTTGCCAATGACGGAACTGGACAGCTTA 272
379 TGAAGGCGATTTTGAATGCGATTTGCCAATGACGGAACTGGACAGCTTA 438
273 ACTAAGCGATTTTGAATGCGATTTGCCAATGACGGAACTGGACAGCTTA 332
439 GAGTTTAAACCAAAAGGAAAGCGATTTGCCAATGACGGAACTGGACAGCTTA 498
333 GAAATTCGACGAAAGATGCTGCGATTCGAAAGGAAAGCGATTTGCCAATGAC 392
499 GCGCGATTTTGAATGCGATTTGCCAATGACGGAACTGGACAGCTTA 558
393 GCAATTAAGGCTGCTTTCGAGAGGCGATTTTCAGATGATGATGCTGTTGATATAC 452
559 AAAGTGAAGCAAGCGGACAGATGTAATGCGATTTGCCAATGACGGAACTGGAC 618
453 AAGCGCGGCTGATGATTAAGAGAAATTTATGCGACCAATGCGATTTGCCAATGAC 512
619 AACCAAGAAATATGAGGATTAACCGATTTGCCAATGACGGAACTGGACAGCTTA 678
513 AACCAAGAAATATGAGGATTAACCGATTTGCCAATGACGGAACTGGACAGCTTA 572
679 AGAGAAATATCCATTCACCTTAATGAGCGGCTGATATCTTTGATGGGACAGATTTG 738

Db 573 AGAGGCGACAACTGCTCCGATGAGTGAATTTTAAACATTTCACAGGGGTAGACT-- 630
QY 739 GATCACTGACGTAGCTTGAGAACAAATATATTAATTCAGAGTACCGGAAGCATGG 798
Db 631 -ATGAGCGCAAAAGCTGAGACACCGCTATCTTCAAGATTCAGAGGAGCGGAAGCATTTGG 669
QY 799 GACTGGGAAGTATAGAGAACGGCACTATGATTAATCTTATGATGAGACATTGAT 858
Db 690 GCCACCGATTTATTAAGAAAACGGTCTTTGATTTATCTCATGTTTGGCGATTTGAC 749
QY 859 ATGATCATTCAGAACTAATCAATGAATTAAGAAATTTGGG 899
Db 750 CATTACACCCGGATGTTGAGCCGAATCAACAATGGGG 790

RESULT 11
CF708585 752 bp mRNA linear EST 16-AUG-2004
LOCUS CCAGY26TR C.neoformans strain JEC21 Cryptococcus neoformans var.
DEFINITION
ACCESSION CF708585
VERSION CF708585.1 GI:41562744
KEYWORDS EST.
SOURCE Cryptococcus neoformans var. neoformans (Filobasidiella neoformans
var. neoformans)
ORGANISM Cryptococcus neoformans var. neoformans
Bukaryota; Fungi; Basidiomycota; Hymenomycetes;
Heterobasidiomycetes; Tremellomycetidae; Tremellales; Tremellaceae;
Filobasidiella.
1 (bases 1 to 752)
Loftus, B.
REFERENCE JEC21 cDNA library
AUTHORS Unpublished (2003)
COMMENT Other_ESTS: CCAGY26TR
Contact: Brendan Loftus
TIGR
Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,
Rockville, MD 20850, USA
Tel: 301-838-3543
Fax: 301-838-0208
Email: crypt@tigr.org
Seq primer: TR.

FEATURES
source
1..752
Location/Qualifiers
/organism="Cryptococcus neoformans var. neoformans"
/mol_type="mRNA"
/strain="JEC21"
/db_xref="taxon:40410"
/clone="CCAGY26"
/note="Vector: pCMVSPORT6; Site 1: NotI EcoRV. The full
length, normalized library was prepared from a variety of
conditions using RNA provided by Joseph Heitman and
Jennifer Lodge"

ORIGIN
Query Match 9.0%; Score 160.6; DB 7; Length 752;
Best Local Similarity 54.3%; Pred. No. 2.6e-32;
Matches 347; Conservative 0; Mismatches 289; Indels 3; Gaps 1;

QY 259 ACCATGATGAGATTTTGAATGATTCATTCGCAAAATGACGGGAACCACTGGAACAGTTA 318
Db 117 ACAATGATGAGATCTTGATGATGATGATGATGATGATGATGATGATGATGATGAT 176
QY 319 CGAGATGACGACCTAACTTAAGAGTAAAGGATTAACGCTGTTGGATTCTCTCGCA 378
Db 177 GAAGAGGAATCCGAAAGACTGGCCAAACATGGCATCACTGCTTGATTTCTCTCCT 236
QY 379 TGAAGGGGAGCTTCGCAAAATGATGTTGGTATGATGATGATGATGATGATGATGAT 438
Db 237 ACTAAAGGCTTACCGCTTAAGGGTACAGATATGATATTTATGATGTTGGGACTTGGGA 296

QY 439 GAGTTTAACCAAAAGGAACCGTCCGTACAAATATGACAAAGAGTCAAGTTCAGAGT 498
Db 297 GATTTCGACCAAGAAAGATCTGTCTGTACCAATATGGGTATCTTAAGAAGATCTTTAAAA 356
QY 499 GCCGTGACATCTTTGAAAAATTAACGGGATTCAAATTATGAGGATGCTGTGATGATCAT 558
Db 357 GCATTTAAGGCTGCTTCTGAGAAGGGCATTTATCACTGATGATGCTGTGATGATCA 416
QY 559 AAAGTGGAGCAGACGGGACAGAGATGTAATGCGGTGGAAGTGAACCGAAGACCGA 618
Db 417 AAGCGCGGCTGATATTAAGAAAGATTTATGACCACATGCTGAGCAAGATTAACCGT 476
QY 619 AACCAAAATATACAGTGAATACACATTTGAAGCAGTGAACGAATTTATTCCTGGA 678
Db 477 AACAGGAAGTGAAGAAATGACACATTTGAAGCTGAGCAAGTTCATTTCTCTGCG 536
QY 679 AAGGAATATACCATTTCCAACTTTAATGCGGTGATCATTTTATGAGGACAGATTGG 738
Db 537 AGAGGCGACAGATCTCCGACATGAAATTTTAAACATTTTCACAGGGGTAGACT-- 594
QY 739 GATCACTGACGTGAGCTTGAGAACAAATATTAATTCAGAGGTACCGGAAAGCATGG 798
Db 595 -ATGACGCAAAAGCTGAGACACCGCTATCTTCAAGATTCAGAGGAGCGGAAGCATTTGG 653
QY 799 GACTGGGAAGTATAGAGAACGGCACTATGATTAATCTTATGATGAGACATTGAT 858
Db 654 GCCACCGATTTATTAAGAAAACGGTCTTTGATTTATCTCATGTTTGGCGATTTGAC 713
QY 859 ATGATCATTCAGAACTAATCAATGAATTAAGAAATTTGG 897
Db 714 CATTACACCCGGATGTTGAGCCGAATCAACAATGG 752

RESULT 12
CF717666 727 bp mRNA linear EST 16-AUG-2004
LOCUS CCAB472TR C.neoformans strain JEC21 Cryptococcus neoformans var.
DEFINITION
ACCESSION CF717666
VERSION CF717666.1 GI:41571825
KEYWORDS EST.
SOURCE Cryptococcus neoformans var. neoformans (Filobasidiella neoformans
var. neoformans)
ORGANISM Cryptococcus neoformans var. neoformans
Bukaryota; Fungi; Basidiomycota; Hymenomycetes;
Heterobasidiomycetes; Tremellomycetidae; Tremellales; Tremellaceae;
Filobasidiella.
1 (bases 1 to 727)
Loftus, B.
REFERENCE JEC21 cDNA library
AUTHORS Unpublished (2003)
COMMENT Other_ESTS: CCAB472TR
Contact: Brendan Loftus
TIGR
Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,
Rockville, MD 20850, USA
Tel: 301-838-3543
Fax: 301-838-0208
Email: crypt@tigr.org
Seq primer: TR.

FEATURES
source
1..727
Location/Qualifiers
/organism="Cryptococcus neoformans var. neoformans"
/mol_type="mRNA"
/strain="JEC21"
/db_xref="taxon:40410"
/clone="CCAB472"
/note="Vector: pCMVSPORT6; Site 1: NotI EcoRV. The full
length, normalized library was prepared from a variety of
conditions using RNA provided by Joseph Heitman and
Jennifer Lodge"

Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,
Rockville, MD 20850, USA
Tel: 301-838-3543
Fax: 301-838-0208
Email: crypt@tigr.org

Qy	259	ACCAATGATGCAGTATTTTGAATGGCATTTGGCCAATGACGGGAACCACTGGAAACAGGTAA	318
Db	144	ACAATGATGCAGTACTTCGAAATGGTAGCGTAAAGGTGGTGTATCAATGGAAAAAGTAT	203
Qy	319	CGAGATGACGACGCTTAATTAAAGATTAAGGAGTTACCGCTGTTTGGATTCTCTCGCA	378
Db	204	GAAGCGCAATCGAAAAGCTGGCCACAATGGGCACTGCTGTGGATTCTCTCTCT	263
Qy	379	TGGAAGGGGACTTTCGAAAATGATGTTGGGTATGGTGCTTATGATTTGTACGATCTTGGT	438
Db	264	ACTTAAAGCTCTTACCCTTAAGGGTACAGGAATATATATTTATGATGTTTGGGACTTTGGGA	323
Qy	439	GAGTTTAAACCAAAAGGGAAACCGTCCGTACAATAATGGCAACAAGAGTCAGTTGGCAAGT	498
Db	324	GAATTCGACAGAAAGAGTCTGTGGGTACCAATGGGGTACTTAAAGAAGTCTTTTAA	383
Qy	499	GCCGTGACATCTTTGAAAAATTAACGGGATTCMAGTTATGGGAGTGTGATGATGATCAT	558
Db	384	GCAATTAAAGCTGCTTTCGAGAAAGGGCATTTACAGTACATTTGATTCGTCTTGAATCAC	443
Qy	559	AAAGGTGAGCAGACGGGACAGAGATGGTAAATCGGTGGAAATGAAACCGAAGCACCGGA	618
Db	444	AAGCCCGGCGCTGATGATTAAGAAAGAAATTTATGCCCACATGGTGGGACGAAATAACCGT	503
Qy	619	AACCAAAATATATAGGTGAATATACCATTTGAACCATGACAGAAATTTGATTTCCCTGGA	678
Db	504	AAACAAGAGATGAGGAGAAATGACAAACATTTGAAGGCTGGACCAAGTTCATTTCCCTGGC	563
Qy	679	AGAGGAATATCCCATTCCACTTTAAATGGCGCTGTATCATTTTGTATGGACAGATTGG	738
Db	564	AGAGGCGACAGATCTCCGACATGAATGGAAATTTTAAACATTTTCACAGGGGTAGACT--	621
Qy	739	GATCAGTCACGTCAGCTTCAGAAACAAAATATATAAATTCAGAGGTACCGGAAGGACATGG	798
Db	622	-ATGACCCAAAGACTGAGACCAACCGTATCTTCAAGATTCAGGGGAGACGGGAGGACATTGG	680
Qy	799	GACTGGGAATGATATATAGAAACGGCACTATGATTAACCTTATGTATGACAGACT	854
Db	681	GCAACCGATGTTGATTAAGAAACGGGTCTTTTGATATCTCATGTGGTCCGATAT	736

Aedes aegypti (yellow fever mosquito)
Aedes aegypti
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Peerygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae; *Aedes*;
Stegomyia.

REFERENCE
1 (bases 1 to 856)
Loftus, B., Shetty, J., Knudson, D. and Severson, D.
BAC end sequencing of *Aedes aegypti*
Unpublished (2003)
Other GSSs: NDL.49D22.SP6
Contact: Brendan Loftus
Department of Eukaryotic Genomics
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-3543
Fax: 301-838-0208
Email: enta@tigr.org
Library was provided by David Severson
Seq primer: 17
Class: BAC ends.

FEATURES
source
Location/Qualifiers
1..856
/organism="Aedes aegypti"
/mol_type="genomic DNA"
/strain="Liverpool"
/db_xref="taxon:7159"
/clone="NDL.49D22"
/note="Notre Dame Liverpool"
/note="Vector: pECRAC1, Site 1: Hind III; The library was
prepared from whole body tissue of newly hatched L1 larvae
by David Severson at the University of Notre Dame and
Hongbin Zhang"

ORIGIN

Query Match 7.1%; Score 126.2; DB 8; Length 856;
Best Local Similarity 48.3%; Pred. No. 6.5e-23;

Matches 384; Conservative 0; Mismatches 408; Indels 3; Gaps 1;

564 TGGAGCAGACGGGACAGATGTGTAATGCGTGAAGTGAACCGAAGCAAGCAACCA 623
5 TGGCGGCGAGAGAAAGACAGGTTCAGTTCAGAGTGAAGCCCAACCGCAACGA 64
624 AGAAATATCAGGTGATACACCTGGAAGCATGAGCAAAATTGATTTCCCTGGAAAGG 683
65 CATCTACGACGAGGCTTCAGCGCGTGCCTACACCGCGCTTCACTTTCCGCGCTCA 124
684 AAATACCATTTCCAACTTAAATGGCGCTGTATCATTTTGGATGGGACAGATTGGATCA 743
125 GGGCGTGATTCAGATTATCTGGATTCACATGCTTACGGCGCGTCAATACGTGA 184
744 GTACGCTAGCTTCAAGAAACAAATATATTAATTCAGG--GTACCGGAAAGCATGGCA 800
185 GCAGCCGAGACGAAAGGGGTTCAAAATCGCCAGCACTATGCGCAGACGCGTGGAA 244
801 CTGGAGATGATATATAGAAAGCGCACTATGATTTACCTATGATGACAGCAATGATAT 860
245 CGATCAGGTGACGACAAAGGCACTACGACTATCTATGAGGGGCGACCGTGGATT 304
861 GATCATCCAGAGTATCATATGAACTTAAATTTGGGAGTTTGTATCAAAATACAT 920
305 CCGCAATACCGCGGTGACGAGAGCTCAAACTCTGGCGCGCTGTGGAAAGCCT 364
921 TAACTAGATGATTAGAAATGAGTGTGAAAATATTAATTAACGCTATACGAGAGA 980
365 GCGGTGAGCGGCTTCGCGCTGAGCGCGCAAGCAATTCGCGCTGTTCTTCAAGA 424
981 TTGGCTAACATGTGGGTAAACACCAAGGTAACCAATGTTTGCATGTCAGATTG 1040
425 GTGGCGGATCAGTGGCGGCGACGACGCGACCTGTTATTTGTGCGCAATACGT 484
1041 GAAATATGACCTTCTGCAATCGAAATCTATTTTAAATTAACCAAGTTGATCACTCGT 1100
485 GTGGCAGATCTGTGCTGCGTCAACATATCATGAGCTGTGACGCGCAAGGATGCT 544
1101 GTTCGATGTTCTCTTCATTAATTTGTACATGATCTAATAGTGTGGCTAATTTGA 1160
545 GTTCGAGTGGCGCTGACCGTGAAGTTTTCATGAGCGCTCGAAACAGGGCGACGCTTGA 604

QY 1161 TATGAGAAATATTTAAATGTTCTGTGTACAAAACACCTATATACAGTCAAT 1220
DB 605 CATGGCGCATCTTCTACCGATACCTTACCGCCCGCATTCGGCCACGCGTAACGT 664
QY 1221 TCTTGATTAACATGACTCTACCGCAGAGAGACATGGAATCTTTGTCATTCGTGTT 1280
DB 665 GGTTCGCAACACGACACCCACCGCTTGCAATCGCTGGAAGCGCGGTGAAACCTGTGTT 724
QY 1281 CAACACCTGCGATATGATTTATTTGACCAAGGAGCAAGTTACCTCGTATTTTA 1340
DB 725 CAACCGCTGGCTTACGCGCTGATCTGTGCGCAACGAGCGTGCCTGCGTGT 784
QY 1341 CGTGATTTACTACGG 1355
DB 785 CCCCCACCTGTATGG 799

RESULT 15
BH377207/c 576 bp DNA linear GSS 10-DEC-2001
LOCUS
DEFINITION AG-ND-109M22.TF ND-TM Anopheles gambiae genomic clone
AG-ND-109M22, genomic survey sequence.
ACCESSION BH377207
VERSION BH377207.1 GI:17323349
KEYWORDS
SOURCE
ORGANISM
Anopheles gambiae (African malaria mosquito)
Anopheles gambiae
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae;
Anopheles.

REFERENCE
1 (bases 1 to 576)
Hong, Y.S., Hogan, J.R., Wang, X., Sarkar, A., Sim, C., Loftus, B.J.,
Ren, C., Huff, E.R., Carlile, J.L., Black, K., Zhang, H.-B.,
Gardner, M.J., and Collins, F.H.

Construction of a BAC library and generation of BAC end
sequence-tagged connectors for genome sequencing of the African
malaria mosquito *Anopheles gambiae*
Mol. Genet. Genomics 268 (6), 720-728 (2003)

JOURNAL
MEDLINE
PUBMED
1265398
Other GSSs: AG-ND-109M22.TR
Contact: Brendan J Loftus
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0208
Fax: 301 838 3543
Email: bjl@tigr.org

This clone is from an *A. gambiae* BAC library (ND-TM) provided by
F.H. Collins and sequenced by The Institute for Genomic Research
(TIGR). The BAC library was generated from *A. gambiae* PEST strain
DNA. All DNA was extracted from DNA from microorganisms that inhabit
the gut. The DNA is derived from mixed sexes of larvae. The BAC
library was constructed at Texas A&M University BAC Center
University, College Station, Texas 77843-2123, USA using a HindIII
partial digest.
Seq primer: M13 For
Class: BAC ends.

FEATURES
source
Location/Qualifiers
1..576
/organism="Anopheles gambiae"
/mol_type="genomic DNA"
/strain="PEST"
/db_xref="taxon:7165"
/clone="AG-ND-109M22"
/clone_lib="ND-TM"
/note="Vector: pECRAC1, Site_1: HindIII"

ORIGIN

Query Match 7.0%; Score 124.6; DB 8; Length 576;
Best Local Similarity 52.4%; Pred. No. 1.6e-22;
Matches 297; Conservative 0; Mismatches 269; Indels 1; Gaps 1;

QY 421 GATTGTACGATCTTGTGAGTTTAAACCAAGGGAACCGTCCGTACAAAATATGGACA 480
 Db 576 GATTATTCGATTTGAGAGAGTTTATCAGAAAGGAGATTTGCACCTAAATATGGAAT 517
 QY 481 AGGAGTCAGTTGCAAGGTCCGTGACATCTTGAATAAATACGGGATTTCAAGTTATGGG 540
 Db 516 AAGGAGGATTTATTTGGCCGTATATAACAGCTTAATAAGTAAAGTATTCAGATATTGCA 457
 QY 541 GATGTCGATGAAT-CATAAAGTGGAGCAGACCGGACAGAGATGTAAATCCGTGA 599
 Db 456 GATATTTACTGAACCTAAAGCTGGCGGTGACGAGCTGCAGAAATTCAGTTGTGGA 397
 QY 600 AGTGAACCGAAGCAACCGAAACCAAGAAATATCAGGTGAATACACCATTTGAAGCATGAGC 659
 Db 396 AGTAAATCCGAAACCGAAATGAGTGACATCGAACCTTTAATATTAAGTCTTACAC 337
 QY 660 GAAATTTGATTTCCCTGGAAGAGAAATACCCATTCCAACCTTAAATGGCGCTGTATCA 719
 Db 336 GAAATTTAATTTTCTGAGAGAAATAGCAGATTCGGAATTTATCTGGATTTTACCTG 277
 QY 720 TTTTGATGGGACAGTTGGGATCAGTCAGTCAGCTTCAGAACAAATATATTAATTGAG 779
 Db 276 TTTTCAGGTGTGAAATGCTGAGAGAAATGATGTATGCAATGATTCGGGTGATCAA 217
 QY 780 AGTACCGGAAAGCATGGGACTGGGAGTAGATATAGAAACGGCACTATGATTACCT 839
 Db 216 TGATTTATGAGATGTTGGATGAAATTTACTGAGTATGAAAGGGGAACTACGATTATCT 157
 QY 840 TATGTATGACAGATTTGATATGATCATCCAGAAATCAATGAACTTAGAAATTTGGGG 899
 Db 156 GATGAATATATGATTAATAATTTCCGAAATCCAAATGTGTGGAGAAATTAGATTACTGGGG 97
 QY 900 AGTTGGTATACAAATATACATTAATCTAGATGATTTGAATCGATGCTGTGAACATAT 959
 Db 96 GAAAGTGTATATGAAACAGATTGATATATATGATGTAGTGTAGTGTAGTGTATTAACATAT 37
 QY 960 TAAATACAGCTATACGAGATTTGGCT 986
 Db 36 TACACCGGCAATTTTAAAGACTGGCT 10

Search completed: May 2, 2005, 20:14:17
 Job time : 4009 secs

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OM protein - protein search, using sw model

Run on: May 2, 2005, 19:07:27 ; Search time 77 Seconds
(without alignments)
2591.797 Million cell updates/sec

Title: US-08-952-741-2

Perfect score: 2862

Sequence: 1 MKLHNRIISVLLTLLAVAV.....ADGKGNFTVNGAVSWVKQ 516

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

A_Geneseq_16Dec04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2862	100.0	516	AAW11326	AAW11326 Alkaline
2	2862	100.0	516	AAE26535	AAE26535 Bacillus
3	2849	99.5	516	AAE35714	AAE35714 Mutant al
4	2713	94.8	485	AAO21000	AAO21000 Bacillus
5	2704	94.5	485	AAW79904	AAW79904 Liquefied
6	2613	91.3	485	AAW31499	AAW31499 Bacillus
7	2613	91.3	485	AAW48260	AAW48260 Bacillus
8	2613	91.3	485	AAW15421	AAW15421 Termanyli-
9	2613	91.3	485	AAW15415	AAW15415 Bacillus
10	2613	91.3	485	AAW25150	AAW25150 Bacillus
11	2613	91.3	485	AAW07391	AAW07391 Wild type
12	2613	91.3	485	AAW07381	AAW07381 Wild type
13	2613	91.3	485	AAW99602	AAW99602 Bacillus
14	2613	91.3	485	AAW99608	AAW99608 Bacillus
15	2613	91.3	485	AAE06933	AAE06933 Bacillus
16	2613	91.3	485	AAU12149	AAU12149 Bacillus
17	2613	91.3	485	AAE47850	AAE47850 Bacillus
18	2613	91.3	485	AAE47850	AAE47850 Bacillus
19	2613	91.3	485	AAE99480	AAE99480 Amino aci
20	2613	91.3	485	AAU92078	AAU92078 Termanyli-
21	2611	91.2	485	AAW12113	AAW12113 Alpha-amy
22	2610	91.2	485	AAW12121	AAW12121 Alpha-amy
23	2610	91.2	485	AAW12099	AAW12099 Alpha-amy
24	2610	91.2	485	AAW12130	AAW12130 Alpha-amy
25	2610	91.2	485	AAW12107	AAW12107 Alpha-amy

26	2610	91.2	485	2	AAW12119	AAW12119 Alpha-amy
27	2610	91.2	485	2	AAW12102	AAW12102 Alpha-amy
28	2610	91.2	485	2	AAW12108	AAW12108 Alpha-amy
29	2610	91.2	485	2	AAW12106	AAW12106 Alpha-amy
30	2610	91.2	485	2	AAW12129	AAW12129 Alpha-amy
31	2610	91.2	485	2	AAW12118	AAW12118 Alpha-amy
32	2610	91.2	485	2	AAW12098	AAW12098 Alpha-amy
33	2610	91.2	485	2	AAW12103	AAW12103 Alpha-amy
34	2610	91.2	485	2	AAW12104	AAW12104 Alpha-amy
35	2610	91.2	485	2	AAW12105	AAW12105 Alpha-amy
36	2610	91.2	485	2	AAW12120	AAW12120 Alpha-amy
37	2610	91.2	485	2	AAW12100	AAW12100 Alpha-amy
38	2609	91.2	485	2	AAW12114	AAW12114 Alpha-amy
39	2609	91.2	485	2	AAW12117	AAW12117 Alpha-amy
40	2608	91.1	485	2	AAW12122	AAW12122 Alpha-amy
41	2608	91.1	485	2	AAW12125	AAW12125 Alpha-amy
42	2608	91.1	485	2	AAW12124	AAW12124 Alpha-amy
43	2608	91.1	485	2	AAW12123	AAW12123 Alpha-amy
44	2608	91.1	485	2	AAW12126	AAW12126 Alpha-amy
45	2608	91.1	485	2	AAW12131	AAW12131 Alpha-amy

ALIGNMENTS

RESULT 1
AAW11326
ID AAW11326 standard; protein; 516 AA.
XX
AC AAW11326;
XX
DT 17-OCT-2003 (revised)
DT 27-AUG-2003 (revised)
DT 11-NOV-1997 (first entry)
XX
DE Alkaline liquefying alpha-amyase.
XX
KW Alkaline liquefying alpha-amyase; Bacillus; alpha-amyase; detergent;
KW starch-related polysaccharide; hydrolysis; enzyme; surfactant resistance;
KW alpha-1,4-glucosidic link; alkalophilic Bacillus; laundry detergent;
KW dish-washing detergent; starch.
XX
OS Bacillus sp; KSM-AP1378.
XX
PN W09700324-A1.
XX
PD 03-JAN-1997.
XX
PE 14-JUN-1996; 96WO-JP001641.
XX
PR 14-JUN-1995; 95JP-00147257.
XX
PA (KAOS) KAO CORP.
XX
PI Hatada Y, Ozaki K, Ara K, Kawai S, Ito S;
XX
DR WPI; 1997-118708/11.
XX
PT N-PSDB; AAT51339.
XX
PT DNA encoding alkaline liquefying alpha-amyase - useful in dish-washing
XX and laundry detergents for removal of starch dirts.
XX
PS Claim 2; Page 23-26; 40pp; English.
XX
PS This sequence represents an alkaline liquefying alpha-amyase. Alpha-
XX amyase is an enzyme that acts on starch-related polysaccharides,
XX hydrolysing the alpha-1,4-glucoside bond of the polysaccharide molecule.
XX Alkaline liquefying alpha-amyases exhibit resistance to surfactants used
XX in detergents, and decompose starch or starch-related polysaccharides in
XX a highly random manner. The Bacillus species KSM-AP1378, from which this
XX sequence was isolated, is an alkalophilic Bacillus strain. It was
XX isolated from soil in the vicinity of the city of Tochihi. The enzyme is
XX useful in improving the efficiency of dish-washing and laundry

CC detergents, particularly on starch diets. (updated on 27-AUG-2003 to
CC correct OS field.) (updated on 17-OCT-2003 to standardise OS field)
XX
SQ Sequence 516 AA;

Query Match	100.0%	Score 2662;	DB 2;	Length 516;
Best Local Similarity	100.0%	Pred. No. 8	1e-226;	
Matches 516;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

QY	1	KCLNHRISVLLTLLLAVALPFPYMTPEQAOHHNGTMMQYFEWHLPNDSGHNRLRD	60
Db	1	MKLNHRISVLLTLLLAVALFPYMTPEQAOHHNGTMMQYFEWHLPNDSGHNRLRD	60
QY	61	DAANLKSQGTATVWLPPEAKGTSONDVCGAYDLDLSEFNQKGTATKYGTRSOLOQAV	120
Db	61	DAANLKSQGTATVWLPPEAKGTSONDVCGAYDLDLSEFNQKGTATKYGTRSOLOQAV	120
QY	121	TSLKNGGQIYGVADVMMNHHKGADGTEMVAAVEYNRSNRNOEISGEYTIEMWTFEPGKG	180
Db	121	TSLKNGGQIYGVADVMMNHHKGADGTEMVAAVEYNRSNRNOEISGEYTIEMWTFEPGKG	180
QY	181	NTHSNFKRWYHFDGTDMDQSRLOKNIYKFRGTGKAMDWEVDIENGATDYMTADIDMD	240
Db	181	NTHSNFKRWYHFDGTDMDQSRLOKNIYKFRGTGKAMDWEVDIENGATDYMTADIDMD	240
QY	241	HPEVINELRNMGVWYTNLTNLNDGFRIDAYKHIKYSTRTDMLTHRVTTGKPMFAVAEFMK	300
Db	241	HPEVINELRNMGVWYTNLTNLNDGFRIDAYKHIKYSTRTDMLTHRVTTGKPMFAVAEFMK	300
QY	301	NDLAAIENYLNKTSNMNHSVFDVPLHAYNLVNASNGYFDMRNILNGSVYQKPIHAATVY	360
Db	301	NDLAAIENYLNKTSNMNHSVFDVPLHAYNLVNASNGYFDMRNILNGSVYQKPIHAATVY	360
QY	361	DNHDSQPEALAESFVQSMFKPLATVALLILRBOGYPFVFGDYXGPTTHGVPSSKSIDPL	420
Db	361	DNHDSQPEALAESFVQSMFKPLATVALLILRBOGYPFVFGDYXGPTTHGVPSSKSIDPL	420
QY	421	LOARQTYAVGTQHDYFDHDDIIIGWTRBGDSSHNSGLATIMSDPGCNKMYVGKHAQO	480
Db	421	LOARQTYAVGTQHDYFDHDDIIIGWTRBGDSSHNSGLATIMSDPGCNKMYVGKHAQO	480
QY	481	VWRDITGNRSGVTINADGMGNFTYNGGAVVYWKQ	516
Db	481	VWRDITGNRSGVTINADGMGNFTYNGGAVVYWKQ	516

XX	RESULT 2
XX	AAE26535
ID	AAE26535 standard; protein, 516 AA.
XX	
AC	AAE26535;
XX	
DT	13-DEC-2002 (first entry)
XX	
DE	Bacillus species KSM-API378 alpha-amylase protein.
XX	
KM	Alpha amylase; alpha-1,4-glucan-4-glycanohydrolase; EC 3.2.1.1;
KW	dishwashing; textile desizing; detergent; paper; starch liquefaction.
KW	laundry; alcohol production; ethanol production; pulp; beer; brewing
KX	sweetener; enzyme.
XX	
OS	Bacillus sp.
XX	
FH	Key
FT	Peptide
FT	Location/Qualifiers
FT	1..31
FT	/label= Signal-peptide
FT	32..516
FT	/note= "Mature KSM-API378 protein"
XX	
PN	WO200231124-A2.
XX	
PD	18-APR-2002.
XX	

PF 12-OCT-2001; 2001WO-DK00668
XX
PR 13-OCT-2000; 2000DK-00001533
PR 23-OCT-2000; 2000US-0242692P
PR 02-OCT-2001; 2001DK-00001442
PR 03-OCT-2001; 2001US-0326752P
XX

PA (NOVO) NOVOZYMES AS.

PI Andersen C;
vv

DR WPI; 2002-463264/49.
DR N-PSDB: AAD44364

XX KSM-K36 or KSM-K3
PT

PT KSN-K36 or KSN-K38 variant from *Bacillus* for cleaning dishes, textile
PT deizing, starch liquefaction and ethanol production has alpha-amylase
PT activity.

PS Disclosure; Page 64-66; 69pp; English.

CC The present invention relates to KSM-K35 or KSM-K38 variant of parent
CC alpha-amylases (alpha-1,4-glucan-4-glucanohydrolases, EC 3.2.1.1) from
CC *Bacillus*. The variants have alpha-amylase activity and exhibit an amino
CC acid alteration such as an insertion, deletion or substitution of the
CC parent alpha-amylase. The variants are useful for washing and/or dis-
CC washing, textile desizing, starch liquefaction and alcohol production,
CC particularly ethanol production. They are also useful as components in
CC detergents for e.g. laundry, dishwashing and hard surface cleaning
CC detergent compositions, in pulp and paper production, in beer making or
CC brewing and in production of sweeteners. The present sequence is *Bacillus*
CC species KSM-AP1378 alpha-amylase protein

SQ Sequence 516 AA;

Query March	100.0%	Score 2862;	DB 5;	Length 516;
Best Local Similarity	100.0%	Pred. No. 8.1e-226;		
Matches 516;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

QY	1	MKLNHRIISVLLTLLLAVALVFPYMTTEPAQHNTNGTMMQYFEMHLFENDGNHNRLD	60
Db	1	MKLNHRIISVLLTLLLAVALVFPYMTTEPAQHNTNGTMMQYFEMHLFENDGNHNRLD	60
QY	61	DAANLKSGKGTAWMPPMAKGTSONDVGYADYDLGEFNOKGTVRTKYGTSQLOQAV	120
Db	61	DAANLKSGKGTAWMPPMAKGTSONDVGYADYDLGEFNOKGTVRTKYGTSQLOQAV	120
QY	121	TSLNKNGIOYVGDVVMNHKGGADGETEMNAVEVNSNNNOEISGEYTIEMTKFDEPGRG	180
Db	121	TSLNKNGIOYVGDVVMNHKGGADGETEMNAVEVNSNNNOEISGEYTIEMTKFDEPGRG	180
QY	181	NTHSNFKRMWHPDGTDMDOGBOLONKIYKFRGTGKAMDWEVDIENGNDYLMYADIDMD	240
Db	181	NTHSNFKRMWHPDGTDMDOGBOLONKIYKFRGTGKAMDWEVDIENGNDYLMYADIDMD	240
QY	241	HPEVYNELRNMGWWTNTLNLDPGRIDLVKHKIYSYTRDMLTHVENTTCKPMPAAVEFK	300
Db	241	HPEVYNELRNMGWWTNTLNLDPGRIDLVKHKIYSYTRDMLTHVENTTCKPMPAAVEFK	300
QY	301	NDLAAIENYLNKTSWNHNSVFDVPLHYNLYNASHSGYFDMRNLNGSVVQKPIHATFEV	360
Db	301	NDLAAIENYLNKTSWNHNSVFDVPLHYNLYNASHSGYFDMRNLNGSVVQKPIHATFEV	360
QY	361	DNHOSQPEALAESFQSWFKPLAVALLLTREGGYSVFQDYGIPTHGVPBMKSIDPL	420
Db	361	DNHOSQPEALAESFQSWFKPLAVALLLTREGGYSVFQDYGIPTHGVPBMKSIDPL	420
QY	421	LOAROTYVYGTQHDYFDHHDIIIGWTRREGDSHPNSGLATIMSDGPGNKMVYQKHKQAQ	480
Db	421	LOAROTYVYGTQHDYFDHHDIIIGWTRREGDSHPNSGLATIMSDGPGNKMVYQKHKQAQ	480
QY	481	VMRDTITGRSGTVTINADMGKFTYNGGAVSVWVWQ	516
Db	481	VMRDTITGRSGTVTINADMGKFTYNGGAVSVWVWQ	516

RESULT 3
AAB35714
ID AAB35714 standard; protein; 516 AA.
XX
AC AAB35714;
XX
DT 19-FEB-2001 (first entry)
XX
DE Mutant alpha-amylase amino acid sequence.
XX
KM Alpha-amylase; detergent; Bacillus.
XX
OS Bacillus sp.
XX
FH Key Location/Qualifiers
FT Misc-difference 297
FT /note= "Represented as Alu in the specification"
FT Misc-difference 335
FT /note= "Represented as Aly in the specification"
XX
PN JP2000245466-A.
XX
PD 12-SEP-2000.
XX
PF 25-FEB-1999; 99JP-00048213.
XX
PR 25-FEB-1999; 99JP-00048213.
XX
PA (KAOS) KAO CORP.
XX
DR WPI: 2000-615143/59.
DR N-PSDB; AAC66234.
XX
PT A novel mutant alpha-amylase for use in a detergent composition.
XX
PS Claim 1; Page 5-6; 12pp; Japanese.
XX
CC The present invention relates to a mutant alpha-amylase. Included in the
CC invention are a gene encoding the mutant alpha-amylase, a vector
CC containing the gene, and a transformed cell recombined by the vector. The
CC enzyme is used in a detergent composition. The present sequence
CC represents the mutant alpha-amylase protein
XX
SQ Sequence 516 AA:
Query Match 99.5%; Score 2849; DB 3; Length 516;
Best Local Similarity 99.6%; Pred. No. 9.4e-225;
Matches 514; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 MCLNRIISVLLTLLAVAVLPYMTPEBAQHNGNGTMMQYFEMHLPNDGNHNRRLD 60
DB 1 MCLNRIISVLLTLLAVAVLPYMTPEBAQHNGNGTMMQYFEMHLPNDGNHNRRLD 60
QY 61 DAALKSKGTAAWIIPAMKGTSONDVGYGAYDIYDGEFQKGTVRKTYGTRSQLQGA 120
DB 61 DAALKSKGTAAWIIPAMKGTSONDVGYGAYDIYDGEFQKGTVRKTYGTRSQLQGA 120
QY 121 TSLKNGNIOYVGDVVMNHKGGADGTEMVNAVEVNRNSNRNOISGEYTIETAWTKFDPG 180
DB 121 TSLKNGNIOYVGDVVMNHKGGADGTEMVNAVEVNRNSNRNOISGEYTIETAWTKFDPG 180
QY 121 TSLKNGNIOYVGDVVMNHKGGADGTEMVNAVEVNRNSNRNOISGEYTIETAWTKFDPG 180
DB 121 TSLKNGNIOYVGDVVMNHKGGADGTEMVNAVEVNRNSNRNOISGEYTIETAWTKFDPG 180
QY 181 NTHSNFPMRWYHFDGTMDQSRQLNKIKYKRGTKAMDEVDIENGNYDYLMADIDMD 240
DB 181 NTHSNFPMRWYHFDGTMDQSRQLNKIKYKRGTKAMDEVDIENGNYDYLMADIDMD 240
QY 181 NTHSNFPMRWYHFDGTMDQSRQLNKIKYKRGTKAMDEVDIENGNYDYLMADIDMD 240
DB 181 NTHSNFPMRWYHFDGTMDQSRQLNKIKYKRGTKAMDEVDIENGNYDYLMADIDMD 240
QY 241 HPEVINELRMNGVWYNTLNDGFRIDAVKHIKSYTRDMLTHVANTTKGMEFAVAFWK 300
DB 241 HPEVINELRMNGVWYNTLNDGFRIDAVKHIKSYTRDMLTHVANTTKGMEFAVAFWK 300
QY 301 NDLAIAENYLNKTSWMNSVDFVPLAHYNLYNASNGGYFDMENILNGSVQKPIHAATFV 360
DB 301 NDLAIAENYLNKTSWMNSVDFVPLAHYNLYNASNGGYFDMENILNGSVQKPIHAATFV 360

DB 301 NDLAIAENYLNKTSWMNSVDFVPLAHYNLYNASNGGYFDMENILNGSVQKPIHAATFV 360
QY 361 DNHSOPGEALIESFVQSMFKPLAVALITREOGYPSVFGYVGIPTHGVSMSKIDPL 420
DB 361 DNHSOPGEALIESFVQSMFKPLAVALITREOGYPSVFGYVGIPTHGVSMSKIDPL 420
QY 421 LQARQTYAGTQHDYFPHHDIIGWTRGDSHSPNSGLATTIMSDPGGNKMMYVGHKRAQ 480
DB 421 LQARQTYAGTQHDYFPHHDIIGWTRGDSHSPNSGLATTIMSDPGGNKMMYVGHKRAQ 480
QY 481 VMRDITGNRSGTGTINADGNGFTVNGGAVSVWVKQ 516
DB 481 VMRDITGNRSGTGTINADGNGFTVNGGAVSVWVKQ 516
RESULT 4
AAO21000
ID AAO21000 standard; protein; 485 AA.
XX
AC AAO21000;
XX
DT 19-JUL-2002 (first entry)
XX
DE Bacillus sp alpha-amylase KSM-API378 (FERM BP-3048) protein.
XX
KM Alpha-amylase; detergent; laundry; bleaching; dishwashing; enzyme;
KM fibre desizing; starch liquefaction; KSM-API378; FERM BP-3048.
XX
OS Bacillus sp.
XX
FH Key Location/Qualifiers
FT Protein 1..485
FT /note= "Mature protein"
XX
PN EP1199356-A2.
XX
PD 24-APR-2002.
XX
PF 10-OCT-2001; 2001EP-00123378.
XX
PR 11-OCT-2000; 2000JP-00310605.
XX
PA (KAOS) KAO CORP.
XX
PI Arai H, Hagihari H, Hayashi Y, Endo K, Igarashi K, Ozaki K;
XX
DR WPI: 2002-354203/39.
DR N-PSDB; AAK99881.
XX
PT New mutant alpha-amylase, useful in detergent compositions, comprises
PT increased productivity when prepared recombinantly and better resistance
PT to heat.
XX
PS Claim 1; Page 16-18; 45pp; English.
XX
CC The invention relates to a mutant alpha-amylase derived from a fully
CC defined sequence of 485 amino acids or a 480 aa sequence as given in the
CC specification by substitution or deletion of one or more specified amino
CC acids. The mutant amylase proteins of the invention can be produced at a
CC high yield from a recombinant organism, making it possible to drastically
CC reduce the cost of their production. The mutant amylase proteins are
CC useful in detergent compositions (e.g. laundry, bleaching and dishwashing
CC compositions), also for liquefaction of starch and desizing fibres,
CC optionally used in conjunction with other enzymes. This sequence
CC represents the 485 amino acid Bacillus sp. alpha-amylase KSM-API378 (FERM
CC BP-3048) protein of the invention
XX
SQ Sequence 485 AA:
Query Match 94.8%; Score 2713; DB 5; Length 485;
Best Local Similarity 100.0%; Pred. No. 1.2e-213;
Matches 485; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 32 HHNGTGMQVPEWHLPNDGNHNRRLRDAALNLSKSGITAWIIPAMKGTSONDVGYGA 91
 DB 1 HHNGTGMQVPEWHLPNDGNHNRRLRDAALNLSKSGITAWIIPAMKGTSONDVGYGA 60
 QY 92 YDLVDLGEFNQKGTAVTKYGTGTSQLOQAVTSLKNNGIQVYGDVVMNHKGGADGTEWNAV 151
 DB 61 YDLVDLGEFNQKGTAVTKYGTGTSQLOQAVTSLKNNGIQVYGDVVMNHKGGADGTEWNAV 120
 QY 152 EVNRSNRNOEISGEYTIETAWTKDFPGRGNTSHNFKRWYHFDGTDWDSROLQNKITYK 211
 DB 121 EVNRSNRNOEISGEYTIETAWTKDFPGRGNTSHNFKRWYHFDGTDWDSROLQNKITYK 180
 QY 212 RGTGKAMDWEVDIENGNYDYLMADIDMDHPEVYNELRNMGVYTYTLNDGFRIDAVKH 271
 DB 181 RGTGKAMDWEVDIENGNYDYLMADIDMDHPEVYNELRNMGVYTYTLNDGFRIDAVKH 240
 QY 272 IKTSYTRDMLTHVRNTGKMPFAVAEFWKNDLAIENYLNKTSWNHSEVDFVPLHYNL 331
 DB 241 IKTSYTRDMLTHVRNTGKMPFAVAEFWKNDLAIENYLNKTSWNHSEVDFVPLHYNL 300
 QY 332 SMSGGYFDMENIINGSVQKHPIHATVPVNNHDSQPEALSFVQSWFKPLAYALLITRE 391
 DB 301 SMSGGYFDMENIINGSVQKHPIHATVPVNNHDSQPEALSFVQSWFKPLAYALLITRE 360
 QY 392 QGYPSVFGDYGIPTHGVPMSKSIDPLLOARQTYAGTQHDYFPHHDIIGTREGDSS 451
 DB 361 QGYPSVFGDYGIPTHGVPMSKSIDPLLOARQTYAGTQHDYFPHHDIIGTREGDSS 420
 QY 452 HPMNSGLATIMSDPGGNKMMYVGGKHAGQVWRDITGNRSGTIVTINADGWNFTVNGGAVS 511
 DB 421 HPMNSGLATIMSDPGGNKMMYVGGKHAGQVWRDITGNRSGTIVTINADGWNFTVNGGAVS 480
 QY 512 VMTVKQ 516
 DB 481 VMTVKQ 485

RESULT 5
 AAM79904
 ID AAM79904 standard; protein; 485 AA.

XX AAM79904;
 AC 18-DEC-1998 (first entry)
 DT
 XX
 DE Liquefied alkaline alpha-amylase.
 KM Liquefied alkaline alpha-amylase; mutation; Bacillus licheniformis;
 KW detergent; bleaching agent; oxidising agent.
 XX
 OS Bacillus licheniformis.
 FH Key Location/Qualifiers
 FT Misc-difference 202 /note= "can be deleted or substituted by another amino
 acid residue such as Thr, Ile, Leu, Ala, Val or Ser"
 FT
 XX
 PN WO9844126-A1.
 PD 08-OCT-1998.
 PF 31-MAR-1998; 98WO-JP001464.
 PR 31-MAR-1997; 97JP-00080299.
 XX
 PA (KAOS) KAO CORP.
 XX
 PI Hatada Y, Ikawa K, Ito S;
 XX
 DR WPI; 1998-542707/46.
 XX
 PT Bacillus derived alpha amylase having mutation at position 202 - has
 optimum pH in alkaline conditions and high tolerance to oxidants, useful

PT for production of detergent compositions.
 XX
 XX Claim 1; Page 19-21; 42pp; Japanese.
 XX
 CC The present sequence represents Bacillus licheniformis liquefied alkaline
 CC alpha-amylase. The present invention describes mutated forms of the
 CC liquefied alkaline alpha-amylase derived from Bacillus species KSM-AP1378
 CC (FERM BP-3048), having the methionine residue at position 202 either
 CC deleted or substituted by another amino acid, such as threonine,
 CC isoleucine, leucine, alanine, valine or serine. The mutated enzyme may
 CC have other mutations (such as deletion of arginine or glycine at
 CC positions 181 and 182, respectively) but at least 95.2% homologous to the
 CC original enzyme. The mutated enzyme has optimum pH in alkaline
 CC conditions, a high alpha amylase activity, and a high and sustained
 CC tolerance to oxidising substances. The enzyme may be used in the
 CC formulation of liquid, powder or granular detergent compositions,
 CC especially those containing bleaches and oxidants. The enzyme retains
 CC high activity in the presence of bleaches and oxidants allowing improved
 CC detergent formulations to be produced
 XX

SO Sequence 485 AA;
 Query Match 94.5%; Score 2704; DB 2; Length 485;
 Best Local Similarity 99.8%; Pred. No. 6,7e-213;
 Matches 484; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 32 HHNGTGMQVPEWHLPNDGNHNRRLRDAALNLSKSGITAWIIPAMKGTSONDVGYGA 91
 DB 1 HHNGTGMQVPEWHLPNDGNHNRRLRDAALNLSKSGITAWIIPAMKGTSONDVGYGA 60
 QY 92 YDLVDLGEFNQKGTAVTKYGTGTSQLOQAVTSLKNNGIQVYGDVVMNHKGGADGTEWNAV 151
 DB 61 YDLVDLGEFNQKGTAVTKYGTGTSQLOQAVTSLKNNGIQVYGDVVMNHKGGADGTEWNAV 120
 QY 152 EVNRSNRNOEISGEYTIETAWTKDFPGRGNTSHNFKRWYHFDGTDWDSROLQNKITYK 211
 DB 121 EVNRSNRNOEISGEYTIETAWTKDFPGRGNTSHNFKRWYHFDGTDWDSROLQNKITYK 180
 QY 212 RGTGKAMDWEVDIENGNYDYLMADIDMDHPEVYNELRNMGVYTYTLNDGFRIDAVKH 271
 DB 181 RGTGKAMDWEVDIENGNYDYLMADIDMDHPEVYNELRNMGVYTYTLNDGFRIDAVKH 240
 QY 272 IKTSYTRDMLTHVRNTGKMPFAVAEFWKNDLAIENYLNKTSWNHSEVDFVPLHYNL 331
 DB 241 IKTSYTRDMLTHVRNTGKMPFAVAEFWKNDLAIENYLNKTSWNHSEVDFVPLHYNL 300
 QY 392 QGYPSVFGDYGIPTHGVPMSKSIDPLLOARQTYAGTQHDYFPHHDIIGTREGDSS 451
 DB 361 QGYPSVFGDYGIPTHGVPMSKSIDPLLOARQTYAGTQHDYFPHHDIIGTREGDSS 420
 QY 452 HPMNSGLATIMSDPGGNKMMYVGGKHAGQVWRDITGNRSGTIVTINADGWNFTVNGGAVS 511
 DB 421 HPMNSGLATIMSDPGGNKMMYVGGKHAGQVWRDITGNRSGTIVTINADGWNFTVNGGAVS 480
 QY 512 VMTVKQ 516
 DB 481 VMTVKQ 485

RESULT 6
 AAM31499
 ID AAM31499 standard; protein; 485 AA.

XX AAM31499;
 AC 08-APR-1998 (first entry)
 DT
 XX
 DE Bacillus sp. alpha amylase.

KW Alpha amylase; hard surface cleaning; dishwashing; laundry.
XX Bacillus sp.
XX WO9732961-A2.
XX 12-SEP-1997.
XX 04-MAR-1997; 97WO-US003635.
XX 07-MAR-1996; 96WO-US003276.
XX (PROC) PROCTER & GAMBLE CO.
XX Baec AC, Jones LA, Ohtani R, Pramod K, Rai S, Showell MS;
XX Ward G;
XX WPI; 1997-457524/42.
XX Detergent compositions for hard surface cleaning and laundry use -
XX PT contains Bacillus derived alpha amylase with improved thermostability,
XX PT reduced calcium ion dependency etc.
XX Claim 1; Page 86-87; 97pp; English.
XX The present sequence is a Bacillus sp. alpha amylase with a specific
XX activity at least 25% higher than that of Termamyl (RTM) at 25 to 55
XX degrees C at pH 8 to 10, measured by the Phadebas (RTM) activity test. It
XX is of use in hard surface cleaning, hand or machine dishwashing and
XX laundry at a temperature of 10 to 25 degrees C. Improved cleaning, stain
XX removal and fabric care are obtained by using it at a concentration of
XX 0.00018 to 0.06%
XX Sequence 485 AA;

Query Match 91.3%; Score 2613; DB 2; Length 485;
Best Local Similarity 95.1%; Pred. No. 1.9e-205;
Matches 461; Conservative 16; Mismatches 8; Indels 0; Gaps 0;
QY 32 HHNGTNGTMQYFEMHLPNDGNHNRRLRDDAANKSKGITAVWIPPAWKGSQNDVGYGA 91
DB 1 HHNGTNGTMQYFEMHLPNDGNHNRRLRDDAANKSKGITAVWIPPAWKGSQNDVGYGA 60
QY 92 YDLVLDGFBNOKGTVRKTYGTRSOLOGAVTSLKNNGIQVGDVYNNHKGADGTEBMNAV 151
DB 61 YDLVLDGFBNOKGTVRKTYGTRNOLOAAVTSLKNNGIQVGDVYNNHKGADGTEIYNAV 120
QY 152 EVNSNRNOISGEYTIEMTKFDPFGKGNTHSNFKRWYHFDGTDMDQSOLOKIKYKF 211
DB 121 EVNSNRNOISGEYTIEMTKFDPFGKGNTHSNFKRWYHFDGTDMDQSOLOKIKYKF 180
QY 212 RGTGKAMWEVDIENGNYDYIMYADIMDHPVINELRNKGWYNTNTLNDGFRIDAVKH 271
DB 181 RGTGKAMWEVDIENGNYDYIMYADIMDHPVINELRNKGWYNTNTLNDGFRIDAVKH 240
QY 272 IKYSYTRDMLTHVNTTGGKPMFAVAEFWKNDLAAIENYLNKTSWNHVSFDPVPLHYNLNA 331
DB 241 IKYSYTRDMLTHVNTTGGKPMFAVAEFWKNDLAAIENYLNKTSWNHVSFDPVPLHYNLNA 300
QY 332 SNSGGYFDMRNILNGSVVQKPHIAVTFVNDHDSQPEALLESFYQSWFKPLAYALITRE 391
DB 301 SNSGGYFDMRNILNGSVVQKPHIAVTFVNDHDSQPEALLESFYQSWFKPLAYALITRE 360
QY 392 QGYPSVFYGDYGGIPTHGVPMSKSIDPLLOARQTYAVGTQHDYFDHDDIIGWTREDDSS 451
DB 361 QGYPSVFYGDYGGIPTHGVPMSKSIDPLLOARQTYAVGTQHDYFDHDDIIGWTREDDSS 420
QY 452 HPNSGLATIMSDGPGKNTVMYVGGKAGQVWRDITGNSSGTVTINADQWGFYNNGAVS 511
DB 421 HPNSGLATIMSDGPGKNTVMYVGGKAGQVWRDITGNSSGTVTINADQWGFYNNGAVS 480
QY 512 VVWVXQ 516
DB |||||

DB 481 VVWVXQ 485
RESULT 7
AAW48260
ID AAW48260 standard; protein; 485 AA.
AC AAW48260;
XX 02-JUL-1998 (first entry)
XX DE Bacillus sp. alpha amylase protein #1.
XX Alpha amylase; stain digestion; detergent; fabric laundry performance.
XX OS Bacillus sp.
XX WO9805748-A1.
XX 12-FEB-1998.
XX 01-AUG-1996; 96WO-US012612.
XX 01-AUG-1996; 96WO-US012612.
XX PR 01-AUG-1996; 96WO-US012612.
XX PA (PROC) PROCTER & GAMBLE CO.
XX PI Baec AC, Jones LA, Ohtani R, Pramod K, Rai S, Showell MS;
XX WPI; 1998-159168/14.
XX Use of specific alpha-amylase enzymes - in laundry detergent compositions
XX to provide effective cleaning and whitening of dingy fabrics.
XX Claim 1; Page 69-70; 82pp; English.
XX This sequence represents an alpha amylase from Bacillus sp. which is used
XX in a laundry detergent. The detergent compositions can be used for
XX boosting fabric laundry performance or for dingy fabric cleanup
XX Sequence 485 AA;

Query Match 91.3%; Score 2613; DB 2; Length 485;
Best Local Similarity 95.1%; Pred. No. 1.9e-205;
Matches 461; Conservative 16; Mismatches 8; Indels 0; Gaps 0;
QY 32 HHNGTNGTMQYFEMHLPNDGNHNRRLRDDAANKSKGITAVWIPPAWKGSQNDVGYGA 91
DB 1 HHNGTNGTMQYFEMHLPNDGNHNRRLRDDAANKSKGITAVWIPPAWKGSQNDVGYGA 60
QY 92 YDLVLDGFBNOKGTVRKTYGTRSOLOGAVTSLKNNGIQVGDVYNNHKGADGTEBMNAV 151
DB 61 YDLVLDGFBNOKGTVRKTYGTRNOLOAAVTSLKNNGIQVGDVYNNHKGADGTEIYNAV 120
QY 152 EVNSNRNOISGEYTIEMTKFDPFGKGNTHSNFKRWYHFDGTDMDQSOLOKIKYKF 211
DB 121 EVNSNRNOISGEYTIEMTKFDPFGKGNTHSNFKRWYHFDGTDMDQSOLOKIKYKF 180
QY 212 RGTGKAMWEVDIENGNYDYIMYADIMDHPVINELRNKGWYNTNTLNDGFRIDAVKH 271
DB 181 RGTGKAMWEVDIENGNYDYIMYADIMDHPVINELRNKGWYNTNTLNDGFRIDAVKH 240
QY 272 IKYSYTRDMLTHVNTTGGKPMFAVAEFWKNDLAAIENYLNKTSWNHVSFDPVPLHYNLNA 331
DB 241 IKYSYTRDMLTHVNTTGGKPMFAVAEFWKNDLAAIENYLNKTSWNHVSFDPVPLHYNLNA 300
QY 332 SNSGGYFDMRNILNGSVVQKPHIAVTFVNDHDSQPEALLESFYQSWFKPLAYALITRE 391
DB 301 SNSGGYFDMRNILNGSVVQKPHIAVTFVNDHDSQPEALLESFYQSWFKPLAYALITRE 360
QY 392 QGYPSVFYGDYGGIPTHGVPMSKSIDPLLOARQTYAVGTQHDYFDHDDIIGWTREDDSS 451
DB 361 QGYPSVFYGDYGGIPTHGVPMSKSIDPLLOARQTYAVGTQHDYFDHDDIIGWTREDDSS 420
QY 512 VVWVXQ 516
DB |||||

QY 452 HPSGLATTMSDGGKMKMYVGNKAKAGVWRDITGNRSTVTITNADGNGFTVNGAVS 511
| | | | |
DB 421 HPSGLATTMSDGGKMKMYVGNKAKAGVWRDITGNRSTVTITNADGNGFTVNGAVS 480
| | | | |
QY 512 VVWKQ 516
| | | | |
DB 481 VVWKQ 485
| | | | |
RESULT 8
ID AAY15421 standard; protein; 485 AA.
AA15421:
AA15421:
22-JUL-1999 (first entry)
Termamyl-like alpha-amylase protein.
Termamyl-like alpha-amylase protein.
Termamyl-like; alpha-amylase; variant; washing; dishwashing; production;
sweetener; ethanol; starch; textile desizing; starch liquefaction;
saccharification process.
Bacillus sp.
MO9923211-A1.
14-MAY-1999.
30-OCT-1998; 98WO-DK000471.
30-OCT-1997; 97DK-00001240.
PR 14-JUL-1998; 98DK-00000936.
XX
XX (NOVO) NOVO-NORDISK AS.
XX
XX Borchert TV, Svendsen A, Andersen C, Nielsen BR, Nissen TL;
PI Kjaerulf S;
DR WPI; 1999-326987/27.
XX
XX New Termamyl-like alpha-amylase variants.
PT
XX Claim 38; Page 88-89; 115pp; English.
XX
XX The specification describes termamyl-like alpha-amylase variants that
CC have altered amino acid sequences to improve properties. The variants are
CC produced by creating one or more of the following mutations in amino acid
CC sequence of the parent termamyl-like alpha-amylase: T141, K142, F143,
CC D144, F145, P146, G147, R148, G149, Q174, R181, G182, D183, G184, K185,
CC A186, W189, S193, N195, H107, K108, G109, D166, W167, D168, Q169, S170,
CC R171, Q172, F173, F267, W268, K269, N270, D271, L272, G273, A274, L275,
CC K311, E346, K385, G456, N457, K458, P459, G460, T461, V462, T463. The
CC variants can be used for washing and/or dishwashing. They can also be
CC used in the production of sweeteners and ethanol from starch, and/or for
CC textile desizing, and in starch liquefaction and/or saccharification
CC processes. The present amylase can function as the parent sequence in the
CC production of the variants of the invention
XX
XX Sequence 485 AA:
SQ
Query Match 91.3%; Score 2613; DB 2; Length 485;
Best Local Similarity 95.1%; Pred. No. 1.9e-205;
Matches 461; Conservative 16; Mismatches 8; Indels 0; Gaps 0;

QY 152 EVNRSNRNOEISGEYTIEMTKPDPPRGNTSNFKNRYHFDGTDMDOSROLONKIYF 211
| | | | |
DB 121 EVNRSNRNOEISGEYTIEMTKPDPPRGNTSNFKNRYHFDGTDMDOSROLONKIYF 180
| | | | |
QY 212 RGTGKAMDEVDIENGNDYLMYADIDMDHPEVINELRNWGVWYTNLTLDGFRIDAVKH 271
| | | | |
DB 181 RGTGKAMDEVDIENGNDYLMYADIDMDHPEVINELRNWGVWYTNLTLDGFRIDAVKH 240
| | | | |
QY 272 IKSTYRDMLTHTNRTTGKPMFPAVAFPMKRDALIENTYLNKTSWNHVSFDPVPLHYLVNA 331
| | | | |
DB 241 IKSTYRDMLTHTNRTTGKPMFPAVAFPMKRDALIENTYLNKTSWNHVSFDPVPLHYLVNA 300
| | | | |
QY 332 SNNGGYFDMRNILNGSVQKPHAVTFVNDHSDQGEALLESFVQSWFPLAYALITRE 391
| | | | |
DB 301 SNNGGYFDMRNILNGSVQKPHAVTFVNDHSDQGEALLESFVQSWFPLAYALITRE 360
| | | | |
QY 392 QGYPSVFGDYDYGIPTHGVPSMKSRIIDPLQARQYAYCTQHDYFPHDIIIGWTREGSS 451
| | | | |
DB 361 QGYPSVFGDYDYGIPTHGVPSMKSRIIDPLQARQYAYCTQHDYFPHDIIIGWTREGSS 420
| | | | |
QY 452 HPSGLATTMSDGGKMKMYVGNKAKAGVWRDITGNRSTVTITNADGNGFTVNGAVS 511
| | | | |
DB 421 HPSGLATTMSDGGKMKMYVGNKAKAGVWRDITGNRSTVTITNADGNGFTVNGAVS 480
| | | | |
QY 512 VVWKQ 516
| | | | |
DB 481 VVWKQ 485
| | | | |
RESULT 9
ID AAY15415 standard; protein; 485 AA.
AA15415:
AA15415:
22-JUL-1999 (first entry)
Bacillus strain NCIB 12512 alpha-amylase protein.
Bacillus strain NCIB 12512 alpha-amylase protein.
Termamyl-like; alpha-amylase; variant; washing; dishwashing; production;
sweetener; ethanol; starch; textile desizing; starch liquefaction;
saccharification process.
Bacillus sp.
MO9923211-A1.
14-MAY-1999.
30-OCT-1998; 98WO-DK000471.
30-OCT-1997; 97DK-00001240.
PR 14-JUL-1998; 98DK-00000936.
XX
XX (NOVO) NOVO-NORDISK AS.
XX
XX Borchert TV, Svendsen A, Andersen C, Nielsen BR, Nissen TL;
PI Kjaerulf S;
DR WPI; 1999-326987/27.
XX
XX New Termamyl-like alpha-amylase variants.
PT
XX Claim 38; Page 77-79; 115pp; English.
XX
XX The specification describes termamyl-like alpha-amylase variants that
CC have altered amino acid sequences to improve properties. The variants are
CC produced by creating one or more of the following mutations in amino acid
CC sequence of the parent termamyl-like alpha-amylase: T141, K142, F143,
CC D144, F145, P146, G147, R148, G149, Q174, R181, G182, D183, G184, K185,
CC A186, W189, S193, N195, H107, K108, G109, D166, W167, D168, Q169, S170,
CC R171, Q172, F173, F267, W268, K269, N270, D271, L272, G273, A274, L275,

CC K311, E346, K385, G456, N457, K458, P459, G460, T461, V462, T463. The
CC variants can be used for washing and/or dishwashing. They can also be
CC used in the production of sweeteners and ethanol from starch, and/or for
CC textile desizing, and in starch liquefaction and/or saccharification
CC processes. The present amylase can function as the parent sequence in the
CC production of the variants of the invention

XX Sequence 485 AA;

Query Match 91.3%; Score 2613; DB 2; Length 485;
Best Local Similarity 95.1%; Pred. No. 1.9e-205;
Matches 461; Conservative 16; Mismatches 8; Indels 0; Gaps 0;

QY 32 HHNGNGTMQYFEEHLLPNDGNHNRRLDDAANKSKGTAVIPPAKGTSONDVGCA 91
DB 1 HHNGNGTMQYFEEHLLPNDGNHNRRLDDAANKSKGTAVIPPAKGTSONDVGCA 60
QY 92 YDLVLDGEFNGKGTVRTKYGTRSQLQCAVTSKKNNGIOYGDVVMNHHKGADGTEMVNAV 151
DB 61 YDLVLDGEFNGKGTVRTKYGTRSQLQCAVTSKKNNGIOYGDVVMNHHKGADGTEMVNAV 120
QY 152 EVNRSNRNOEISGEYTIETAWTKFDPFGKGNTHSNFKRWYHFDGTDMDQSRLQNKIKYF 211
DB 121 EVNRSNRNOEISGEYTIETAWTKFDPFGKGNTHSNFKRWYHFDGTDMDQSRLQNKIKYF 180
QY 212 RGTGKAMWEVDIENGNDYLMYADIDMDHPEVINELRNKGVWYNTNTLNGFRIDAVKH 271
DB 181 RGTGKAMWEVDIENGNDYLMYADIDMDHPEVINELRNKGVWYNTNTLNGFRIDAVKH 240
QY 272 IKYSTRLDMLTHVNTTGGKPMFAVAEFWKNDLAIENYLNKTSNMHSYFDPVPLHNLVNA 331
DB 241 IKYSTRLDMLTHVNTTGGKPMFAVAEFWKNDLAIENYLNKTSNMHSYFDPVPLHNLVNA 300
QY 332 SNSGGYFDMRNILNGSVVQKHPHIAVTFVDNHSQPGBALESFVQSWFKPLAVALITRE 391
DB 301 SNSGGYFDMRNILNGSVVQKHPHIAVTFVDNHSQPGBALESFVQSWFKPLAVALITRE 360
QY 392 QGYSVFYGDDYGGIPTHGVPMKSKIDPLQARQTFAGTQHDYFDHDDIIGWTEGSS 451
DB 361 QGYSVFYGDDYGGIPTHGVPMKSKIDPLQARQTFAGTQHDYFDHDDIIGWTEGSS 420
QY 452 HPNSGLATIMSDGPGKMKMYGKHKAGQVWRDITGNRSQVTINADGNGFTVNGAVS 511
DB 421 HPNSGLATIMSDGPGKMKMYGKHKAGQVWRDITGNRSQVTINADGNGFTVNGAVS 480
QY 512 VVWQK 516
DB 481 VVWQK 485

RESULT 10
AA25150
ID AA25150 standard; protein; 485 AA.

AC AA25150;

DT 27-AUG-1999 (first entry)

DE Bacillus sp. alpha-amylase protein fragment 1.

XX Alpha-amylase; cleaning composition; protease variant; spot removal;
XX detergent composition; hard surface cleaning; fabric cleaning;
XX dishwashing composition; oral cleaning composition; personal cleansing;
XX stain removal; soil removal; whiteness maintenance; dingy cleanup;
XX film removal.

XX Bacillus sp.

OS WO9920723-A2.

XX 29-APR-1999.

XX 23-OCT-1998; 98WO-US022486.

XX 23-OCT-1997; 97US-00956323.
PR 23-OCT-1997; 97US-00956324.
PR 23-OCT-1997; 97US-00956554.
XX (PROC) PROCTER & GAMBLE CO.

PI Ghosh CK, Baack AC, Ohtani R, Busch A, Showell MS;

DR WPI; 1999-404706/34.

PT Cleaning compositions used in e.g. detergent for cleaning hard surfaces
PT or fabrics, dishwashing or oral cleaning comprises protease and amylase
PT variants having amino acid residues.

PS Claim 1b(11); Page 164-165; 169pp; English.

CC This invention describes novel cleaning compositions which contain a
CC protease variant with an amino acid substitution corresponding to
CC position 103 of Bacillus amyloliquefaciens and an alpha-amylase variant.
CC The compositions can be used in e.g. detergent compositions, for cleaning
CC hard surfaces or fabrics, dishwashing compositions, oral cleaning
CC compositions, detergent cleaning compositions and personal cleansing
CC compositions. The combination of protease variants and alpha-amylase
CC variants in cleaning compositions can provide improved and enhanced
CC cleaning ability, including stain and/or soil removal and/or reduction
CC and/or whiteness maintenance and/or dingy cleanup and/or spot and/or film
CC removal and/or reduction, over conventional enzyme-containing cleaning
CC compositions

XX Sequence 485 AA;

Query Match 91.3%; Score 2613; DB 2; Length 485;
Best Local Similarity 95.1%; Pred. No. 1.9e-205;
Matches 461; Conservative 16; Mismatches 8; Indels 0; Gaps 0;

QY 32 HHNGNGTMQYFEEHLLPNDGNHNRRLDDAANKSKGTAVIPPAKGTSONDVGCA 91
DB 1 HHNGNGTMQYFEEHLLPNDGNHNRRLDDAANKSKGTAVIPPAKGTSONDVGCA 60
QY 92 YDLVLDGEFNGKGTVRTKYGTRSQLQCAVTSKKNNGIOYGDVVMNHHKGADGTEMVNAV 151
DB 61 YDLVLDGEFNGKGTVRTKYGTRSQLQCAVTSKKNNGIOYGDVVMNHHKGADGTEMVNAV 120
QY 152 EVNRSNRNOEISGEYTIETAWTKFDPFGKGNTHSNFKRWYHFDGTDMDQSRLQNKIKYF 211
DB 121 EVNRSNRNOEISGEYTIETAWTKFDPFGKGNTHSNFKRWYHFDGTDMDQSRLQNKIKYF 180
QY 212 RGTGKAMWEVDIENGNDYLMYADIDMDHPEVINELRNKGVWYNTNTLNGFRIDAVKH 271
DB 181 RGTGKAMWEVDIENGNDYLMYADIDMDHPEVINELRNKGVWYNTNTLNGFRIDAVKH 240
QY 272 IKYSTRLDMLTHVNTTGGKPMFAVAEFWKNDLAIENYLNKTSNMHSYFDPVPLHNLVNA 331
DB 241 IKYSTRLDMLTHVNTTGGKPMFAVAEFWKNDLAIENYLNKTSNMHSYFDPVPLHNLVNA 300
QY 332 SNSGGYFDMRNILNGSVVQKHPHIAVTFVDNHSQPGBALESFVQSWFKPLAVALITRE 391
DB 301 SNSGGYFDMRNILNGSVVQKHPHIAVTFVDNHSQPGBALESFVQSWFKPLAVALITRE 360
QY 392 QGYSVFYGDDYGGIPTHGVPMKSKIDPLQARQTFAGTQHDYFDHDDIIGWTEGSS 451
DB 361 QGYSVFYGDDYGGIPTHGVPMKSKIDPLQARQTFAGTQHDYFDHDDIIGWTEGSS 420
QY 452 HPNSGLATIMSDGPGKMKMYGKHKAGQVWRDITGNRSQVTINADGNGFTVNGAVS 511
DB 421 HPNSGLATIMSDGPGKMKMYGKHKAGQVWRDITGNRSQVTINADGNGFTVNGAVS 480
QY 512 VVWQK 516
DB 481 VVWQK 485

RESULT 11
 AAY07391 standard; protein; 485 AA.
 ID AAY07391 standard; protein; 485 AA.
 XX AAY07391;
 AC AAY07391;
 DT 16-JUL-1999 (first entry)
 DE Wild type Termamy1 (RTM)-like alpha-amylase protein #7.
 XX Variant; Termamy1; alpha-amylase; mutation; Bacillus; detergent;
 KW dishwashing; laundry; textile; desizing; starch liquefaction; sweetener;
 KM ethanol.
 XX Bacillus sp.
 OS Bacillus sp.
 XX MO9919467-A1.
 XX 22-APR-1999.
 XX 13-OCT-1998; 98WO-DK000444.
 XX 13-OCT-1997; 97DK-00001172.
 XX (NOVO) NOVO-NORDISK AS.
 XX Svendsen A, Borchert TV, Bisgard-Frantzen H;
 XX WPI; 1999-277632/23.
 XX Variant alpha-amylases - useful as detergents or for textile desizing or
 PT starch liquefaction.
 XX Disclosure; Page 72-74; 93pp; English.
 PS This sequence represents the parent sequence for new variants of a parent
 XX Termamy1-like alpha-amylase with alpha-amylase activity. The variants
 CC comprise mutations in 2-6 regions/positions relative to an alpha-amylase
 CC from either of two Bacillus species in WO9526397, B. stearothermophilus,
 CC B. licheniformis, B. amyloliquefaciens or Bacillus sp. #707. The alpha-
 CC amylase variants are detergent additives for use in detergents for
 CC dishwashing, manual or automatic laundry. The variants can also be used
 CC for textile desizing or starch liquefaction (e.g. for production of
 CC sweeteners or ethanol)
 CC Sequence 485 AA;
 SQ
 Query Match 91.3%; Score 2613; DB 2; Length 485;
 Best Local Similarity 95.1%; Pred. No. 1.9e-205;
 Matches 461; Conservative 16; Mismatches 8; Indels 0; Gaps 0;
 QY 32 HHNGTNGTMMGYFEWHLPLNDGNHNRRLDDAANKSKGTLAVWIPPAWKGTSQNDVGYGA 91
 DB 1 HHNGTNGTMMGYFEWHLPLNDGNHNRRLDDAANKSKGTLAVWIPPAWKGTSQNDVGYGA 60
 QY 92 YDLVLDGFPNQKGTIRTKYGRSOLQGAVTSLKNNGLIOVGDVNNHKGADGTEMNAV 151
 DB 61 YDLVLDGFPNQKGTIRTKYGRSOLQGAVTSLKNNGLIOVGDVNNHKGADGTEMNAV 120
 QY 152 EYVNRNROEISGEYTIEMWTFDPFGKNTSHNFKRMWYHFDGTDWQSOLOKIKYKF 211
 DB 121 EYVNRNROEISGEYTIEMWTFDPFGKNTSHNFKRMWYHFDGTDWQSOLOKIKYKF 180
 QY 212 RGTGAMDEVDIENGNDYIMYADIDMDHPEVINELKNNGWYTNLTNLDFGRIDAVKH 271
 DB 181 RGTGAMDEVDIENGNDYIMYADIDMDHPEVINELKNNGWYTNLTNLDFGRIDAVKH 240
 QY 272 IKYSTTRMLTHVRNTTGGPMFAVAEPKNDLALENTLNTKSNHSHVEDPLAHNLNA 331
 DB 241 IKYSTTRMLTHVRNTTGGPMFAVAEPKNDLALENTLNTKSNHSHVEDPLAHNLNA 300
 QY 332 SNSGVPDRNLNLSVVOKEPIHVAFTVDNHSQGEALBSFVQSWFKPLAVALITRE 391

DB 301 SNSGVPDRNLNLSVVOKEPIHVAFTVDNHSQGEALBSFVQSWFKPLAVALITRE 360
 QY 392 QGYPSVFPGDYIGITRGPSPKSKIDPLQARQTYAAGTQHDYDCHDIIIGMTRGDS 451
 DB 361 QGYPSVFPGDYIGITRGPSPKSKIDPLQARQTYAAGTQHDYDCHDIIIGMTRGDS 420
 QY 452 HPSGLATTMSDGPCKMVMYGGKAKQVWRDITGNRSGTITINADGNGFTVNGAVS 511
 DB 421 HPSGLATTMSDGPCKMVMYGGKAKQVWRDITGNRSGTITINADGNGFTVNGAVS 480
 QY 512 VWVWQ 516
 DB 481 VWVWQ 485
 RESULT 12
 AAY07381
 ID AAY07381 standard; protein; 485 AA.
 XX AAY07381;
 AC AAY07381;
 DT 16-JUL-1999 (first entry)
 DE Wild type Termamy1 (RTM)-like alpha-amylase protein #1.
 XX Variant; Termamy1; alpha-amylase; mutation; Bacillus; detergent;
 KW dishwashing; laundry; textile; desizing; starch liquefaction; sweetener;
 KM ethanol.
 XX Bacillus sp.
 OS Bacillus sp.
 XX Key Location/Qualifiers
 FH Misc-difference 181..184
 FT /note="optionally 1, 2, 3 or all residues are deleted"
 FT Misc-difference 195
 FT /note="optionally altered to any amino acid except an
 FT Asn residue"
 FT Misc-difference 206
 FT /note="optionally altered to any amino acid except a Val
 FT residue"
 FT Misc-difference 212
 FT /note="optionally altered to any amino acid except a Glu
 FT residue"
 FT Misc-difference 216
 FT /note="optionally altered to any amino acid except a Glu
 FT residue"
 FT Misc-difference 269
 FT /note="optionally altered to any amino acid except a Lys
 FT residue"
 XX MO9919467-A1.
 XX 22-APR-1999.
 XX 13-OCT-1998; 98WO-DK000444.
 XX 13-OCT-1997; 97DK-00001172.
 XX (NOVO) NOVO-NORDISK AS.
 XX Svendsen A, Borchert TV, Bisgard-Frantzen H;
 XX WPI; 1999-277632/23.
 XX Variant alpha-amylases - useful as detergents or for textile desizing or
 PT starch liquefaction.
 PS Claim 1; Page 61-63; 93pp; English.
 XX This sequence represents the parent sequence for new variants of a parent
 CC Termamy1-like alpha-amylase with alpha-amylase activity. The variants
 CC comprise mutations in 2-6 regions/positions relative to an alpha-amylase
 CC from either of two Bacillus species in WO9526397, B. stearothermophilus,

CC B. licheniformis, B. amyloliquefaciens or Bacillus sp. #707. The alpha-
CC amylase variants are detergent additives for use in detergents for
CC dishwashing, manual or automatic laundry. The variants can also be used
CC for textile desizing or starch liquefaction (e.g. for production of
CC sweeteners or ethanol)

XX Sequence 485 AA;

Query Match 91.3%; Score 2613; DB 2; Length 485;

Best Local Similarity 95.1%; Pred. No. 1.9e-205; Matches 461; Conservative 16; Mismatches 8; Indels 0; Gaps 0;

```
QY 32 HHNGTNGTMQYFEWHLFNDGNHNRRLDDANLKSKITAVWIPPAKGTSONDVGYGA 91
DB 1 HHNGTNGTMQYFEWHLFNDGNHNRRLDDANLKSKITAVWIPPAKGTSONDVGYGA 60
QY 92 YDLVDLGEFNQKGVTRTKYGRNQLOAAVTSLKNNGIQVYGDVVMNHKGADGTEIVNAV 151
DB 61 YDLVDLGEFNQKGVTRTKYGRNQLOAAVTSLKNNGIQVYGDVVMNHKGADGTEIVNAV 120
QY 152 EVNSNRNROEISGEYTIEMTKFDFPGRGNTSHNFKRWYHFDGTDMDQSRLOKIKYKF 211
DB 121 EVNSNRNROEISGEYAIEMTKFDFPGRGNNHSSFKRWYHFDGTDMDQSRLOKIKYKF 180
QY 212 RGTGKAMDMEVDIENGNDYLMYADIDMDHEVINELRNMGVWYNTNTLNDGFRIDAVKH 271
DB 181 RGTGKAMDMEVDIENGNDYLMYADIDMDHEVINELRNMGVWYNTNTLNDGFRIDAVKH 240
QY 272 IKYSTTRDMLTHVNTTCKPMPFAVAEFWKNDLAIENLNTKSNHSEFVDPPLHNLVNA 331
DB 241 IKYSTTRDMLTHVNTTCKPMPFAVAEFWKNDLAIENLNTKSNHSEFVDPPLHNLVNA 300
QY 332 SNSGGYFPMRNILNGSVVQKPIHATVFDVNDHDSQPGALBSFYQSWKPKPLAYALVLTRE 391
DB 301 SNSGGYFPMRNILNGSVVQKPIHATVFDVNDHDSQPGALBSFYQSWKPKPLAYALVLTRE 360
QY 392 QGYPSVFYGDYYGIPTHGVPSPKSKIDPLDAROTYAGTQHDYFDHDDIIGMTRREGSS 451
DB 361 QGYPSVFYGDYYGIPTHGVPSPKSKIDPLDAROTYAGTQHDYFDHDDIIGMTRREGSS 420
QY 452 HPNSGLATIMSDGPGNKMVYGVKHKAGQVWRDITGNRS GTVTINADGMGNFTVNGAVS 511
DB 421 HPNSGLATIMSDGPGNKMVYGVKHKAGQVWRDITGNRS GTVTINADGMGNFTVNGAVS 480
QY 512 VVWVKQ 516
DB 481 VVWVKQ 485
```

RESULT 13

AA99602 ID AA99602 standard; protein; 485 AA.

AA99602;

04-SEP-2000 (first entry)

Bacillus parent Termamyl-like alpha-amylase #1.

Bacillus; alpha-amylase; washing; textile desizing; starch liquefaction;
KW saccharification; muten; mutant; enzyme stability; hybrid.

Bacillus sp.

MO200029560-A1.

25-MAY-2000.

16-NOV-1999; 99WO-DK000628.

16-NOV-1998; 98DK-00001495.

(NOVO) NOVO-NORRISK AS.

XX Svendsen A, Kjaerulf S, Biegaard-Frantzen H, Andersen C;
PI WPI: 2000-38777/73.
XX N-PSDB; AAA48480.

Variant of parent termamyl-like alpha amylase useful for washing, textile
desizing and starch liquefaction, comprising alterations in one or more
solvent exposed amino acid residues.

Claim 8, Page 53-54; 80pp; English.

The present sequence is a parent Termamyl-like alpha-amylase from which
mutants with increased stability at acidic pH, low calcium concentration
and high temperatures have been derived. The sequence encoding this
protein was isolated from a Bacillus genomic DNA library. A variant may
contain mutations in one or more solvent exposed amino acid residues to
increase the overall hydrophobicity of the enzyme or the overall number
of methyl groups in the side chains of exposed residues may be increased.
The mutations can be incorporated by site-directed mutagenesis or by
random mutagenesis. As a result of their increased stability, the
CC variants are suitable for the industrial processing of starch, i.e.
CC starch liquefaction and saccharification. They may also be useful for
CC washing, dishwashing and textile desizing. Hybrid alpha-amylases
CC comprising partial amino acid sequences derived from two or more alpha-
CC amylases have also been created in order to increase enzyme stability

Sequence 485 AA;

Query Match 91.3%; Score 2613; DB 3; Length 485;

Best Local Similarity 95.1%; Pred. No. 1.9e-205; Matches 461; Conservative 16; Mismatches 8; Indels 0; Gaps 0;

```
QY 32 HHNGTNGTMQYFEWHLFNDGNHNRRLDDANLKSKITAVWIPPAKGTSONDVGYGA 91
DB 1 HHNGTNGTMQYFEWHLFNDGNHNRRLDDANLKSKITAVWIPPAKGTSONDVGYGA 60
QY 92 YDLVDLGEFNQKGVTRTKYGRNQLOAAVTSLKNNGIQVYGDVVMNHKGADGTEIVNAV 151
DB 61 YDLVDLGEFNQKGVTRTKYGRNQLOAAVTSLKNNGIQVYGDVVMNHKGADGTEIVNAV 120
QY 152 EVNSNRNROEISGEYTIEMTKFDFPGRGNTSHNFKRWYHFDGTDMDQSRLOKIKYKF 211
DB 121 EVNSNRNROEISGEYAIEMTKFDFPGRGNNHSSFKRWYHFDGTDMDQSRLOKIKYKF 180
QY 212 RGTGKAMDMEVDIENGNDYLMYADIDMDHEVINELRNMGVWYNTNTLNDGFRIDAVKH 271
DB 181 RGTGKAMDMEVDIENGNDYLMYADIDMDHEVINELRNMGVWYNTNTLNDGFRIDAVKH 240
QY 272 IKYSTTRDMLTHVNTTCKPMPFAVAEFWKNDLAIENLNTKSNHSEFVDPPLHNLVNA 331
DB 241 IKYSTTRDMLTHVNTTCKPMPFAVAEFWKNDLAIENLNTKSNHSEFVDPPLHNLVNA 300
QY 332 SNSGGYFPMRNILNGSVVQKPIHATVFDVNDHDSQPGALBSFYQSWKPKPLAYALVLTRE 391
DB 301 SNSGGYFPMRNILNGSVVQKPIHATVFDVNDHDSQPGALBSFYQSWKPKPLAYALVLTRE 360
QY 392 QGYPSVFYGDYYGIPTHGVPSPKSKIDPLDAROTYAGTQHDYFDHDDIIGMTRREGSS 451
DB 361 QGYPSVFYGDYYGIPTHGVPSPKSKIDPLDAROTYAGTQHDYFDHDDIIGMTRREGSS 420
QY 452 HPNSGLATIMSDGPGNKMVYGVKHKAGQVWRDITGNRS GTVTINADGMGNFTVNGAVS 511
DB 421 HPNSGLATIMSDGPGNKMVYGVKHKAGQVWRDITGNRS GTVTINADGMGNFTVNGAVS 480
QY 512 VVWVKQ 516
DB 481 VVWVKQ 485
```

RESULT 14

AA99608 ID AA99608 standard; protein; 485 AA.

XX AAY93608;
 XX 04-SEP-2000 (first entry)
 XX Bacillus Termamyl-like alpha-amylase.
 XX Bacillus; alpha-amylase; washing; textile desizing; starch liquefaction;
 XX saccharification; muten; mutant; enzyme stability; hybrid.
 XX Bacillus sp.
 XX MO200029560-A1.
 XX 25-MAY-2000.
 XX 16-NOV-1999; 99WO-DK000628.
 XX 16-NOV-1998; 98DK-00001495.
 XX (NOVO) NOVO-NORDISK AS.
 XX Svendsen A, Kjaerulf S, Bisgard-Frantzen H, Andersen C;
 XX WPI; 2000-387777/33.
 XX Variant of parent termamyl-like alpha amylase useful for washing, textile
 XX desizing and starch liquefaction, comprising alterations in one or more
 XX solvent exposed amino acid residues.
 XX Claim 8; Page 62-64; 80pp; English.
 XX The present sequence is a parent alpha-amylase from which mutants with
 XX increased stability at acidic pH, low calcium concentration and high
 XX temperatures have been derived. The sequence encoding this enzyme was
 XX isolated from a Bacillus genomic DNA library. A variant may contain
 XX mutations in one or more solvent exposed amino acid residues to increase
 XX the overall hydrophobicity of the enzyme or the overall number of methyl
 XX groups in the side chains of exposed residues may be increased. The
 XX mutations can be incorporated by site-directed mutagenesis or by random
 XX mutagenesis. As a result of their increased stability, the variants are
 XX suitable for the industrial processing of starch, i.e. starch
 XX liquefaction and saccharification. They may also be useful for washing,
 XX dishwashing and textile desizing. Hybrid alpha-amylases comprising
 XX partial amino acid sequences derived from two or more alpha-amylases have
 XX also been created in order to increase enzyme stability
 XX Sequence 485 AA;
 SQ
 Query Match 91.3%; Score 2613; DB 3; Length 485;
 Best Local Similarity 95.1%; Pred. No. 1.9e-205;
 Matches 461; Conservative 16; Mismatches 8; Indels 0; Gaps 0;
 QY 32 HHNGTNGTMMQYFEWHLNDGNHNNRLRDDAANLKSQITAWIIPRAKGTSONDVGGA 91
 DB 1 HHNGTNGTMMQYFEWHLNDGNHNNRLRDDAANLKSQITAWIIPRAKGTSONDVGGA 60
 QY 92 YDIYDLCGEFQKGTVRKGTGTSQLOCAVTSLKONGIQVYGDVVMNHKGGADGTEWNAV 151
 DB 61 YDIYDLCGEFQKGTVRKGTGTSQLOCAVTSLKONGIQVYGDVVMNHKGGADGTEWNAV 120
 QY 152 EVNRSNRNCGEISGEYITEATKTFDFPGRGTHSNFKRWYHPFGTMDQSGROKNTIKYK 211
 DB 121 EVNRSNRNCGEISGEYITEATKTFDFPGRGTHSNFKRWYHPFGTMDQSGROKNTIKYK 180
 QY 212 RGTGKAMDEVDIENGNYDYIADIDMDPEVINEIRNMGVYTYTINLDGFRIDAVK 271
 DB 181 RGTGKAMDEVDIENGNYDYIADIDMDPEVINEIRNMGVYTYTINLDGFRIDAVK 240
 QY 272 IKKSYTRDWLTHVRNTTGKMPFAVEFWKNDLAIENYLNKTSWNISVPRPPLHYLYNA 331
 DB 241 IKKSYTRDWLTHVRNTTGKMPFAVEFWKNDLAIENYLNKTSWNISVPRPPLHYLYNA 300
 SQ

QY 332 SNSGGYEDMRNLINGSVOKPHAVTFVDNHDSDGCEALIESFVQSMFKPLAVALLTRE 391
 DB 301 SNSGGYEDMRNLINGSVOKPHAVTFVDNHDSDGCEALIESFVQSMFKPLAVALLTRE 360
 QY 392 QGYPSVFYGDYGIPTHGVPMSKSKIDPLLOARQTYAVGTQHDYFDHDIIGWTRBGSS 451
 DB 361 QGYPSVFYGDYGIPTHGVPMSKSKIDPLLOARQTYAVGTQHDYFDHDIIGWTRBGSS 420
 QY 452 HPRSGLATMSDGPNGKRWYGVKHAQGVWMDITGNRSGTYTINADGNGFTVNGGAAS 511
 DB 421 HPRSGLATMSDGPNGKRWYGVKHAQGVWMDITGNRSGTYTINADGNGFTVNGGAAS 480
 QY 512 VWYKQ 516
 DB 481 VWYKQ 485
 RESULT 15
 ABB06933
 ID ABB06933 standard; protein; 485 AA.
 XX ABB06933;
 XX 19-JUN-2002 (first entry)
 XX Bacillus termamyl-like alpha-amylase protein SEQ ID NO:2.
 XX Bacillus; termamyl-like alpha-amylase; alpha-amylase; EC 3.2.1.1;
 XX variant; mutant; enzyme; protein co-ordinate data; cleaning; detergent;
 XX washing; sweetener; ethanol; starch.
 XX Bacillus sp.
 XX MO200166712-A2.
 XX 13-SEP-2001.
 XX 07-MAR-2001; 2001WO-DK000144.
 XX 08-MAR-2000; 2000DK-00000376.
 XX 15-MAR-2000; 2000US-0189837P.
 XX 23-FEB-2001; 2001DK-00000303.
 XX 26-FEB-2001; 2001US-0271382P.
 XX (NOVO) NOVOZYMES AS.
 XX Andersen C, Borchert TV, Nielsen BR;
 XX WPI; 2002-239612/29.
 XX N-PADB; ABL50564.
 XX Novel variant of parent termamyl-like alpha-amylase useful as a component
 XX in washing and dishwashing compositions, for textile desizing, for starch
 XX liquefaction, and for producing sweeteners and ethanol from starch.
 XX Claim 8; Page 132-133; 153pp; English.
 XX The present invention describes a variant of a parent termamyl-like alpha
 XX -amylase (EC 3.2.1.1) (I) comprising an alteration at one or more
 XX positions of a group of 31 possible amino acid positions. The alteration
 XX in (I) may be at Arg28, Arg118, Asn174, Arg181, Gly182, Asp183, Gly184,
 XX Gly186, Trp189, Asn185, Met202, Tyr298, Asn299, Lys302, Ser303, Asn306,
 XX Arg310, Asn314, Arg320, His324, Glu345, Tyr396, Arg400, Trp439, Arg444,
 XX Asn445, Lys446, Glu449, Arg458, Asn471, or Asn484. (I) can be used for
 XX washing and/or dishwashing, textile desizing, and starch liquefaction.
 XX (I) is useful as a component in hard surface cleaning detergent
 XX composition, and for producing sweeteners and ethanol from starch. (I)
 XX has altered solubility, preferably increased solubility, in particular
 XX under washing, dish washing or hard surface cleaning conditions. The
 XX present sequence represents a Bacillus termamyl-like alpha-amylase which
 XX is used in the exemplification of the present invention
 XX Sequence 485 AA;
 SQ

Query Match 91.3%; Score 2613; DB 5; Length 485;
 Best Local Similarity 95.1%; Pred. No. 1.9e-205;
 Matches 461; Conservative 16; Mismatches 8; Indels 0; Gaps 0;

Qy	32	HHNGTNGTMQYFEWHLFNDGNHNRRLDDAANKSKGITAAMIIPPAWKGTSONDVGYGA	91
Db	1	HHNGTNGTMQYFEWYLPNDGNHNRRLDDAANKSKGITAAMIIPPAWKGTSONDVGYGA	60
Qy	92	YDLVDLGEFNKGTVRTKYGTSRQAGAVTSLKXNGIOVGDVYNNHKGADGTEMNAV	151
Db	61	YDLVDLGEFNKGTVRTKYGTSRQAGAVTSLKXNGIOVGDVYNNHKGADGTEIVNAV	120
Qy	152	EVNSNRNQEISGEYTIEMTKFDPFGKNTSHNFKRMYPDGTMDQSRQLOKIKYKF	211
Db	121	EVNSNRNQETSSEVAITPAWTKFDPFGKNNHSSFKRMYPHDGTMDQSRQLOKIKYKF	180
Qy	212	RGTGKAMDWEVDIENGNYDLYMADIDMDHPEVINELRNMGWYNTNTLNLDFRIDAVKH	271
Db	181	RGTGKAMDWEVDTEGNYDLYMADVDMDHPEVIHELNRMGWYNTNTLNLDFRIDAVKH	240
Qy	272	IKYSTRDMLTHVNTTGGKMPAFAEFWKNDLAIENYLNKTSNNHSVFDPPLHYNLYNA	331
Db	241	IKYSTRDMLTHVNTTGGKMPAFAEFWKNDLAIENYLNKTSNNHSVFDPPLHYNLYNA	300
Qy	332	SNSGYPDMRNIILNGSVYQKPIHAVTFVDNHDSDQGEALBSFVQSWFKPLAYALLTRE	391
Db	301	SNSGYPDMRNIILNGSVYQKPIHAVTFVDNHDSDQGEALBSFVQSWFKPLAYALLTRE	360
Qy	392	QGYPSVFYGDYGGIPTHGVPMSKSIDPLQARQTYAGTQHDYFDHDIIGWTREGDSS	451
Db	361	QGYPSVFYGDYGGIPTHGVPMSKSIDPLQARQTYAGTQHDYFDHDIIGWTREGDSS	420
Qy	452	HPNSGLATIMSDGCGNKMVVGKKGAVWRDITGNRSCTVTINADGNGFTVNGGAVS	511
Db	421	HPNSGLATIMSDGCGNKMVVGKKGAVWRDITGNRTGTVTINADGNGFTVNGGGSVS	480
Qy	512	VMVKQ 516	
Db	481	VMVKQ 485	

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 Job time : 80 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 2, 2005, 21:41:18 ; Search time 24 Seconds
(without alignments)
1604.955 Million cell updates/sec

Title: US-08-952-741-2
Perfect score: 2862
Sequence: 1 MKLHNRILSVLTLLAVAV.....ADGWNFTVNGAVSWVKQ 516

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2862	100.0	516	US-09-986-676A-2	Sequence 2, Appli
2	2862	100.0	516	US-09-971-611-2	Sequence 2, Appli
3	2713	94.8	485	US-09-291-023A-18	Sequence 16, Appli
4	2713	94.8	485	US-09-381-687-1	Sequence 1, Appli
5	2713	94.8	485	US-09-340-715A-18	Sequence 18, Appli
6	2613	91.3	485	US-08-446-803-1	Sequence 1, Appli
7	2613	91.3	485	US-08-861-837-1	Sequence 1, Appli
8	2613	91.3	485	US-08-600-908A-12	Sequence 12, Appli
9	2613	91.3	485	US-08-663-838A-12	Sequence 12, Appli
10	2613	91.3	485	US-08-600-656-1	Sequence 1, Appli
11	2613	91.3	485	US-09-170-670-1	Sequence 1, Appli
12	2613	91.3	485	US-09-170-670-7	Sequence 1, Appli
13	2613	91.3	485	US-09-193-068-1	Sequence 7, Appli
14	2613	91.3	485	US-09-193-068-7	Sequence 7, Appli
15	2613	91.3	485	US-09-183-412-1	Sequence 1, Appli
16	2613	91.3	485	US-09-183-412-7	Sequence 7, Appli
17	2613	91.3	485	US-09-354-191A-1	Sequence 1, Appli
18	2613	91.3	485	US-09-291-023A-19	Sequence 19, Appli
19	2613	91.3	485	US-09-290-734-1	Sequence 7, Appli
20	2613	91.3	485	US-09-290-734-7	Sequence 7, Appli
21	2613	91.3	485	US-09-636-252A-12	Sequence 12, Appli
22	2613	91.3	485	US-09-381-687-2	Sequence 2, Appli
23	2613	91.3	485	US-09-545-586-1	Sequence 1, Appli
24	2613	91.3	485	US-09-545-586-7	Sequence 7, Appli
25	2613	91.3	485	US-09-540-715A-19	Sequence 19, Appli
26	2613	91.3	485	US-09-769-864-1	Sequence 1, Appli
27	2613	91.3	485	US-09-769-864-7	Sequence 7, Appli

28	2609	91.2	485	3	US-09-264-097-7	Sequence 7, Appli
29	2598.5	90.8	486	4	US-09-381-687-4	Sequence 4, Appli
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31	2440	85.3	485	2	US-08-861-837-2	Sequence 2, Appli
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34	2440	85.3	485	3	US-09-170-670-8	Sequence 8, Appli
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36	2440	85.3	485	3	US-09-193-068-8	Sequence 8, Appli
37	2440	85.3	485	3	US-09-183-412-2	Sequence 2, Appli
38	2440	85.3	485	3	US-09-183-412-8	Sequence 8, Appli
39	2440	85.3	485	3	US-09-264-097-5	Sequence 5, Appli
40	2440	85.3	485	3	US-09-354-191A-2	Sequence 2, Appli
41	2440	85.3	485	3	US-09-290-734-2	Sequence 2, Appli
42	2440	85.3	485	3	US-09-290-734-8	Sequence 8, Appli
43	2440	85.3	485	4	US-09-381-687-3	Sequence 3, Appli
44	2440	85.3	485	4	US-09-545-586-2	Sequence 2, Appli
45	2440	85.3	485	4	US-09-545-586-8	Sequence 8, Appli

ALIGNMENTS

RESULT 1
US-09-986-676A-2
Sequence 2, Application US/09986676A
Patent No. 6638748
GENERAL INFORMATION:
APPLICANT: HATADA, Yuji
APPLICANT: OZAKI, Katsuya
APPLICANT: ARA, Katsutoshi
APPLICANT: KAWAI, Shuji
APPLICANT: ITO, Susumu
TITLE OR INVENTION: Gene Encoding Alkaline Liquefying Alpha-Amylase
FILE REFERENCE: 2173-0121P
CURRENT APPLICATION NUMBER: US/09/986, 676A
CURRENT FILING DATE: 2001-11-09
PRIOR APPLICATION NUMBER: PCT/JP96/01641
PRIOR FILING DATE: 1996-06-14
PRIOR APPLICATION NUMBER: Japan 147257/1995
PRIOR FILING DATE: 1995-06-14
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PatentIn version 3.1
SEQ ID NO: 2
LENGTH: 516
TYPE: PRT
ORGANISM: Bacillus sp.
US-09-986-676A-2

Query Match 100.0%; Score 2862; DB 4; Length 516;
Best Local Similarity 100.0%; Pred. No. 1.1e-250;
Matches 516; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MKLHNRILSVLTLLAVAVLPYMTBPAQHNGTGMQYFEKMLPNDGNHNRIRD	60
DB	1	MKLHNRILSVLTLLAVAVLPYMTBPAQHNGTGMQYFEKMLPNDGNHNRIRD	60
QY	61	DAANLKSQGITVAWIPPAWPGTSQNDVGYGAYDLYDGEFNQGTVAATKGTSSQLOGAV	120
DB	61	DAANLKSQGITVAWIPPAWPGTSQNDVGYGAYDLYDGEFNQGTVAATKGTSSQLOGAV	120
QY	121	TSLNKNGIQYGGVYVNMHKGADGTEKVNAVEVRSNRNOISGEYTIEMTKDFPGRG	180
DB	121	TSLNKNGIQYGGVYVNMHKGADGTEKVNAVEVRSNRNOISGEYTIEMTKDFPGRG	180
QY	181	NTSNFQKRYHFDGTDMDOSROLNKTYKFGKQKAWDEVIDENGNYYLWYADIDMD	240
DB	181	NTSNFQKRYHFDGTDMDOSROLNKTYKFGKQKAWDEVIDENGNYYLWYADIDMD	240
QY	241	HPEVINELRWGQWYNTNLNDGFRIDAVGHIKYSYTRDWLTHVRNTTGKMPFAVAEFWK	300
DB	241	HPEVINELRWGQWYNTNLNDGFRIDAVGHIKYSYTRDWLTHVRNTTGKMPFAVAEFWK	300

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DB 301 NDAALENTKNTSMNSHVEDVPLHNLNANSGGFPMRNLINSVVOKPIHATV 360
QY 361 DNHDSPGEALLESFVQSWFKPLAYALILTRBOGYPVFGDYGIPTHGVPMSKSIDPL 420
DB 361 DNHDSPGEALLESFVQSWFKPLAYALILTRBOGYPVFGDYGIPTHGVPMSKSIDPL 420
QY 421 LQARQTYAGTODHYFDHDDIIGMTREBDSHPNSGLATIMSDPGGNKMYVGKHAQ 480
DB 421 LQARQTYAGTODHYFDHDDIIGMTREBDSHPNSGLATIMSDPGGNKMYVGKHAQ 480
QY 481 VWRDITGNRSCTVTINADGNGFTTNAGAVSVWVKQ 516
DB 481 VWRDITGNRSCTVTINADGNGFTTNAGAVSVWVKQ 516

RESULT 2
US-09-971-611-2
Sequence 2, Application US/09971611
Patent No. 6743616
GENERAL INFORMATION:
APPLICANT: ARAKI, HIROYUKI
APPLICANT: ENDO, KEIJI
APPLICANT: HAGIHARA, HIROSHI
APPLICANT: IGARASHI, KAZUKI
APPLICANT: HAYASHI, YASUHIRO
APPLICANT: OZAKI, KATSUYA
TITLE OF INVENTION: HIGHLY PRODUCTIVE ALPHA-AMYLASES
FILE REFERENCE: 214377US0
CURRENT APPLICATION NUMBER: US/09/971, 611
CURRENT FILING DATE: 2001-10-09
PRIOR APPLICATION NUMBER: JP 2000/310605
PRIOR FILING DATE: 2001-10-11
NUMBER OF SEQ ID NOS: 51
SOFTWARE: Patentin version 3.1
SEQ ID NO 2
LENGTH: 516
TYPE: PRT
ORGANISM: Bacillus sp. KSM-AP1378
US-09-971-611-2

Query Match 100.0%; Score 2862; DB 4; Length 516;

Best Local Similarity 100.0%; Pred. No. 1.1e-250; Indels 0; Gaps 0;

Matches 516; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKLHNRISVLTLLLAVALFPYMTPEPAQAHNGTGMQYFEMHLFNDGNHNRRLRD 60
DB 1 MKLHNRISVLTLLLAVALFPYMTPEPAQAHNGTGMQYFEMHLFNDGNHNRRLRD 60
QY 61 DAANLSKGIITAWIPPAWGTSONDVGYGAYDLYDGEFNOKGTATKGTSSQOGAV 120
DB 61 DAANLSKGIITAWIPPAWGTSONDVGYGAYDLYDGEFNOKGTATKGTSSQOGAV 120
QY 121 TSJKNNGIOYGVGVNMHKGADGTEWNAVEVNRSRNOEISGEYTIEMTFEFPFGRG 180
DB 121 TSJKNNGIOYGVGVNMHKGADGTEWNAVEVNRSRNOEISGEYTIEMTFEFPFGRG 180
QY 181 NTHSNFMRWYHFDGTDWDSROLOKTIYKFGTGKADWEVDIENGNYDLYMYADIDMD 240
DB 181 NTHSNFMRWYHFDGTDWDSROLOKTIYKFGTGKADWEVDIENGNYDLYMYADIDMD 240
QY 241 HPEVINELRWGWYNTLNLDFRIDAVYGIKSYTRDMLTHVRNTTGKPMFAVAFWK 300
DB 241 HPEVINELRWGWYNTLNLDFRIDAVYGIKSYTRDMLTHVRNTTGKPMFAVAFWK 300
QY 301 NDAALENTKNTSMNSHVEDVPLHNLNANSGGFPMRNLINSVVOKPIHATV 360
DB 301 NDAALENTKNTSMNSHVEDVPLHNLNANSGGFPMRNLINSVVOKPIHATV 360
QY 361 DNHDSPGEALLESFVQSWFKPLAYALILTRBOGYPVFGDYGIPTHGVPMSKSIDPL 420
DB 361 DNHDSPGEALLESFVQSWFKPLAYALILTRBOGYPVFGDYGIPTHGVPMSKSIDPL 420

QY 421 LQARQTYAGTODHYFDHDDIIGMTREBDSHPNSGLATIMSDPGGNKMYVGKHAQ 480
DB 421 LQARQTYAGTODHYFDHDDIIGMTREBDSHPNSGLATIMSDPGGNKMYVGKHAQ 480
QY 481 VWRDITGNRSCTVTINADGNGFTTNAGAVSVWVKQ 516
DB 481 VWRDITGNRSCTVTINADGNGFTTNAGAVSVWVKQ 516

RESULT 3
US-09-291-023A-18
Sequence 18, Application US/09291023A
Patent No. 630871
GENERAL INFORMATION:
APPLICANT: Outtrup, Helle
APPLICANT: Borchert, Torben
APPLICANT: Nielsen, Bjarne
APPLICANT: Nielsen, Vibeke
APPLICANT: Hoeck, Lisbeth
TITLE OF INVENTION: Polypeptides Having Alkaline Alpha-amylose Activity And Nucleic Ac
FILE REFERENCE: 5821.010-US
CURRENT APPLICATION NUMBER: US/09/291, 023A
CURRENT FILING DATE: 1999-04-13
PRIOR APPLICATION NUMBER: DK 1999 00438
PRIOR FILING DATE: 1999-03-31
NUMBER OF SEQ ID NOS: 21
SOFTWARE: Patentin version 3.0
SEQ ID NO 18
LENGTH: 485
TYPE: PRT
ORGANISM: Bacillus
US-09-291-023A-18

Query Match 94.8%; Score 2713; DB 3; Length 485;

Best Local Similarity 100.0%; Pred. No. 3.2e-237; Indels 0; Gaps 0;

Matches 485; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 32 HNGTNGTMMQYFEMHLFNDGNHNRRLRDAAANLSKGIITAWIPPAWGTSONDVGYG 91
DB 1 HNGTNGTMMQYFEMHLFNDGNHNRRLRDAAANLSKGIITAWIPPAWGTSONDVGYG 91
QY 92 YDLYDGEFNOKGTATKGTSSQOGAVTSJKNNGIOYGVGVNMHKGADGTEWNAV 151
DB 92 YDLYDGEFNOKGTATKGTSSQOGAVTSJKNNGIOYGVGVNMHKGADGTEWNAV 151
QY 121 EVNRSRNOEISGEYTIEMTFEFPFGRGNTSHNFWYHFDGTDWDSROLOKTIYK 180
DB 121 EVNRSRNOEISGEYTIEMTFEFPFGRGNTSHNFWYHFDGTDWDSROLOKTIYK 180
QY 212 RGTGKADWEVDIENGNYDLYMYADIDMDHPEVINELRWGWYNTLNLDFRIDAVH 271
DB 212 RGTGKADWEVDIENGNYDLYMYADIDMDHPEVINELRWGWYNTLNLDFRIDAVH 271
QY 272 IKSYTRDMLTHVRNTTGKPMFAVAFWKNDLAAIENYLNKNTSMNSHVEDVPLHNLN 331
DB 272 IKSYTRDMLTHVRNTTGKPMFAVAFWKNDLAAIENYLNKNTSMNSHVEDVPLHNLN 331
QY 332 SNSGGFDMRNLINSVVOKPIHATVFNHDSPGEALLESFVQSWFKPLAYALILTR 391
DB 332 SNSGGFDMRNLINSVVOKPIHATVFNHDSPGEALLESFVQSWFKPLAYALILTR 391
QY 392 QGYPSVFGDYGIPTHGVPMSKSIDPLQARQTYAGTODHYFDHDDIIGMTREBDS 451
DB 392 QGYPSVFGDYGIPTHGVPMSKSIDPLQARQTYAGTODHYFDHDDIIGMTREBDS 451
QY 452 HPSGLATTMSDPPGNKMYVGKHAQGYWRDITGNRSCTVTINADGNGFTTNAGAVS 511
DB 452 HPSGLATTMSDPPGNKMYVGKHAQGYWRDITGNRSCTVTINADGNGFTTNAGAVS 511
QY 512 VWVKQ 516
DB 512 VWVKQ 516

Db 481 VVWQ 485

RESULT 4
US-09-381-687-1
; Sequence 1, Application US/09381687
; Patent No. 6486113
; GENERAL INFORMATION:
; APPLICANT: HATADA, Yoji
; APPLICANT: IKAWA, Kaori
; APPLICANT: ITO, Susumu
; APPLICANT: IGARASHI, Kazuaki
; APPLICANT: HAGIHARA, Hiroshi
; APPLICANT: HAYASHI, Yasuhiro
; APPLICANT: ARAKI, Hiroyuki
; APPLICANT: OZAKI, Katsuya
; TITLE OF INVENTION: MUTANT ALPHA-AMYLASES
; FILE REFERENCE: 2173-011SP
; CURRENT APPLICATION NUMBER: US/09/381,687
; CURRENT FILING DATE: 1999-09-23
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 1
; LENGTH: 485
; TYPE: PR1
; ORGANISM: Bacillus sp. KSM-AP 1378
US-09-381-687-1

Query Match 94.8%; Score 2713; DB 4; Length 485;
Best Local Similarity 100.0%; Pred. No. 3.2e-237;
Matches 485; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 32 HHNTNGTMMQYFEMHLPNDGNHNRRLDDAANKSKGITAVWLPAPAKGTSQNDVGGA 91
Db 1 HHNTNGTMMQYFEMHLPNDGNHNRRLDDAANKSKGITAVWLPAPAKGTSQNDVGGA 60

Qy 92 YDLVDLGEFNQKGVTRTKYGRSLOGAVTSLKNGGIQVGDVVMNHKGADGTEMNVA 151
Db 61 YDLVDLGEFNQKGVTRTKYGRSLOGAVTSLKNGGIQVGDVVMNHKGADGTEMNVA 120

Qy 152 EVNRSNNOEISGEYITEAMTKPDFPGRGNTSNFKRWYHFDGTDMDQSRQLONKIYKF 211
Db 121 EVNRSNNOEISGEYITEAMTKPDFPGRGNTSNFKRWYHFDGTDMDQSRQLONKIYKF 180

Qy 212 RGCKAMDWEVDLNGNVDYLMYADIMDHPVINELRNMGVWYTNLTLDGFRIDAVKH 271
Db 181 RGCKAMDWEVDLNGNVDYLMYADIMDHPVINELRNMGVWYTNLTLDGFRIDAVKH 240

Qy 272 IKSYTRDMLTHVNTTGKPMFAVAEFKNDLAIENYLNKTSNHSVFDPVPLHYNLYNA 331
Db 241 IKSYTRDMLTHVNTTGKPMFAVAEFKNDLAIENYLNKTSNHSVFDPVPLHYNLYNA 300

Qy 332 SNSGGEFDMENILNGSVVQKHPHIAVTFVDNHSQPEGALESFVQSWFKPLAYALLITRE 391
Db 301 SNSGGEFDMENILNGSVVQKHPHIAVTFVDNHSQPEGALESFVQSWFKPLAYALLITRE 360

Qy 392 QGYPSVFGDYGGIPTHGVPSMSKIDPLQARQTYAVGQHDYFDHDDIIGWTRREGDSS 451
Db 361 QGYPSVFGDYGGIPTHGVPSMSKIDPLQARQTYAVGQHDYFDHDDIIGWTRREGDSS 420

Qy 452 HPNSGLATTINSDGFGKMMYVVGKKGAVWRDITGRSGVTITNADGNGFTVNGGAVS 511
Db 421 HPNSGLATTINSDGFGKMMYVVGKKGAVWRDITGRSGVTITNADGNGFTVNGGAVS 480

Qy 512 VVWQ 516
Db 481 VVWQ 485

RESULT 5
US-09-540-715A-18
; Sequence 18, Application US/09540715A
; Patent No. 6623948

; GENERAL INFORMATION:
; APPLICANT: Outterup, Helle
; APPLICANT: Borchert, Torben
; APPLICANT: Nielsen, Bjarne
; APPLICANT: Nielsen, Vibeke
; APPLICANT: Hoeck, Lisbeth
; TITLE OF INVENTION: Polypeptides Having Alkaline Alpha-amyase Activity And Nucleic A
; FILE REFERENCE: 5821.010-US
; CURRENT APPLICATION NUMBER: US/09/540,715A
; CURRENT FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/291,023
; PRIOR FILING DATE: 2001-08-14
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 18
; LENGTH: 485
; TYPE: PR1
; ORGANISM: Bacillus
US-09-540-715A-18

Query Match 94.8%; Score 2713; DB 4; Length 485;
Best Local Similarity 100.0%; Pred. No. 3.2e-237;
Matches 485; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 32 HHNTNGTMMQYFEMHLPNDGNHNRRLDDAANKSKGITAVWLPAPAKGTSQNDVGGA 91
Db 1 HHNTNGTMMQYFEMHLPNDGNHNRRLDDAANKSKGITAVWLPAPAKGTSQNDVGGA 60

Qy 92 YDLVDLGEFNQKGVTRTKYGRSLOGAVTSLKNGGIQVGDVVMNHKGADGTEMNVA 151
Db 61 YDLVDLGEFNQKGVTRTKYGRSLOGAVTSLKNGGIQVGDVVMNHKGADGTEMNVA 120

Qy 152 EVNRSNNOEISGEYITEAMTKPDFPGRGNTSNFKRWYHFDGTDMDQSRQLONKIYKF 211
Db 121 EVNRSNNOEISGEYITEAMTKPDFPGRGNTSNFKRWYHFDGTDMDQSRQLONKIYKF 180

Qy 212 RGCKAMDWEVDLNGNVDYLMYADIMDHPVINELRNMGVWYTNLTLDGFRIDAVKH 271
Db 181 RGCKAMDWEVDLNGNVDYLMYADIMDHPVINELRNMGVWYTNLTLDGFRIDAVKH 240

Qy 272 IKSYTRDMLTHVNTTGKPMFAVAEFKNDLAIENYLNKTSNHSVFDPVPLHYNLYNA 331
Db 241 IKSYTRDMLTHVNTTGKPMFAVAEFKNDLAIENYLNKTSNHSVFDPVPLHYNLYNA 300

Qy 332 SNSGGEFDMENILNGSVVQKHPHIAVTFVDNHSQPEGALESFVQSWFKPLAYALLITRE 391
Db 301 SNSGGEFDMENILNGSVVQKHPHIAVTFVDNHSQPEGALESFVQSWFKPLAYALLITRE 360

Qy 392 QGYPSVFGDYGGIPTHGVPSMSKIDPLQARQTYAVGQHDYFDHDDIIGWTRREGDSS 451
Db 361 QGYPSVFGDYGGIPTHGVPSMSKIDPLQARQTYAVGQHDYFDHDDIIGWTRREGDSS 420

Qy 452 HPNSGLATTINSDGFGKMMYVVGKKGAVWRDITGRSGVTITNADGNGFTVNGGAVS 511
Db 421 HPNSGLATTINSDGFGKMMYVVGKKGAVWRDITGRSGVTITNADGNGFTVNGGAVS 480

Qy 512 VVWQ 516
Db 481 VVWQ 485

RESULT 6
US-08-446-803-1
; Sequence 1, Application US/08446803
; Patent No. 5824531
; GENERAL INFORMATION:
; APPLICANT: Outterup, Helle
; APPLICANT: Bisgaard-Frantzen, Henrik
; APPLICANT: Ostergaard, Peter Rahbek
; APPLICANT: Rasmussen, Michael Dolberg
; APPLICANT: Van Der Zee, Pia
; TITLE OF INVENTION: Alkaline Bacillus Amylase

NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSER: No. 58245310 No. 5824531disk of No. 5824531ch America
STREET: 405 Lexington Avenue
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10174
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/446,803
FILING DATE: 01-June-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Harrington, James J.
REGISTRATION NUMBER: 38,711
REFERENCE/DOCKET NUMBER: 4157,204-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 867-0123
TELEFAX: (212) 878-9655
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 485 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-446-803-1

Query Match 91.3%; Score 2613; DB 2; Length 485;
Best Local Similarity 95.1%; Pred. No. 3,7e-228;
Matches 461; Conservative 16; Mismatches 8; Indels 0; Gaps 0;
QY 32 HHNGTGMQYFEMHLPNDGNHNRRLRDDAANKSKGITAWIPAMKGTSONDVGYGA 91
DB 1 HHNGTGMQYFEMHLPNDGNHNRRLRDDAANKSKGITAWIPAMKGTSONDVGYGA 60
QY 92 YDLYDGEFNQKGTATKYGTRSQLQAVTSLKNGIQQYGDVVMHKGADGTEWNAV 151
DB 61 YDLYDGEFNQKGTATKYGTRSQLQAVTSLKNGIQQYGDVVMHKGADGTEWNAV 120
QY 152 EVNRSNRNOEISGEYITAEATKDFPGRGNTHSNFKRWYHFDGTDWDSROLQNKIYK 211
DB 121 EVNRSNRNOEISGEYITAEATKDFPGRGNTHSNFKRWYHFDGTDWDSROLQNKIYK 180
QY 212 RGTGKADWEVDIENGNYDLYMAYADIDMDHPEVINELRWGWYTTTLMDGFRIDAVKH 271
DB 181 RGTGKADWEVDIENGNYDLYMAYADIDMDHPEVINELRWGWYTTTLMDGFRIDAVKH 240
QY 272 IKTSYTRDLTHVRNTTGKPMFAVAFEMKNDLAIENYLNKTSWNSVDPVPLHYLYNA 331
DB 241 IKTSYTRDLTHVRNTTGKPMFAVAFEMKNDLAIENYLNKTSWNSVDPVPLHYLYNA 300
QY 332 SNGGTFPMENIINGSVYQKPHIAVTVDNHDSPGEALSFYQSFKFLAYALLITRE 391
DB 301 SNGGTFPMENIINGSVYQKPHIAVTVDNHDSPGEALSFYQSFKFLAYALLITRE 360
QY 392 QGPAVFYGYGIPHTGVPMSKSIDLLQARQYAVGTOHDFPDHDIIGWTRBDDG 451
DB 361 QGPAVFYGYGIPHTGVPMSKSIDLLQARQYAVGTOHDFPDHDIIGWTRBDDG 420
QY 452 HPSGLATTISDPSGKMKMYVGHKAKAGVYARDITGNRSCTVTINADGMGNFTVNGAVS 511
DB 421 HPSGLATTISDPSGKMKMYVGHKAKAGVYARDITGNRSCTVTINADGMGNFTVNGAVS 480
QY 512 VWTQ 516
DB 481 VWTQ 485

RESULT 7
US-08-861-837-1
Sequence 1, Application US/08661837
Patent No. 5856164
GENERAL INFORMATION:
APPLICANT: Otturup, Helle
APPLICANT: Bisgaard-Frantzen, Henrik
APPLICANT: Ostergaard, Peter Rahbek
APPLICANT: Rasmussen, Michael Dolberg
APPLICANT: Van der Zee, Pia
TITLE OF INVENTION: Alkaline Bacillus Amylase
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSER: No. 58561640 No. 5856164disk of No. 5856164ch America
STREET: 405 Lexington Avenue
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10174
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/861,837
FILING DATE: 01-June-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/446,803
FILING DATE: 01-June-1995
ATTORNEY/AGENT INFORMATION:
NAME: Harrington, James J.
REGISTRATION NUMBER: 38,711
REFERENCE/DOCKET NUMBER: 4157,204-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 867-0123
TELEFAX: (212) 878-9655
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 485 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-861-837-1
Query Match 91.3%; Score 2613; DB 2; Length 485;
Best Local Similarity 95.1%; Pred. No. 3,7e-228;
Matches 461; Conservative 16; Mismatches 8; Indels 0; Gaps 0;
QY 32 HHNGTGMQYFEMHLPNDGNHNRRLRDDAANKSKGITAWIPAMKGTSONDVGYGA 91
DB 1 HHNGTGMQYFEMHLPNDGNHNRRLRDDAANKSKGITAWIPAMKGTSONDVGYGA 60
QY 92 YDLYDGEFNQKGTATKYGTRSQLQAVTSLKNGIQQYGDVVMHKGADGTEWNAV 151
DB 61 YDLYDGEFNQKGTATKYGTRSQLQAVTSLKNGIQQYGDVVMHKGADGTEWNAV 120
QY 152 EVNRSNRNOEISGEYITAEATKDFPGRGNTHSNFKRWYHFDGTDWDSROLQNKIYK 211
DB 121 EVNRSNRNOEISGEYITAEATKDFPGRGNTHSNFKRWYHFDGTDWDSROLQNKIYK 180
QY 212 RGTGKADWEVDIENGNYDLYMAYADIDMDHPEVINELRWGWYTTTLMDGFRIDAVKH 271
DB 181 RGTGKADWEVDIENGNYDLYMAYADIDMDHPEVINELRWGWYTTTLMDGFRIDAVKH 240
QY 272 IKTSYTRDLTHVRNTTGKPMFAVAFEMKNDLAIENYLNKTSWNSVDPVPLHYLYNA 331
DB 241 IKTSYTRDLTHVRNTTGKPMFAVAFEMKNDLAIENYLNKTSWNSVDPVPLHYLYNA 300
QY 332 SNGGTFPMENIINGSVYQKPHIAVTVDNHDSPGEALSFYQSFKFLAYALLITRE 391

Db 301 SMSGYVPMRNLNGSVVQKPHAVTFVDNHDSPGEBALSFVQWFKPLAVALVLTRE 360
Qy 392 QGYSPVFYGDYGGIPTHGVPBMKSKIDPLQARQTYAVGTQHDYFDHDDIIGWTRREGDSS 451
Db 361 QGYSPVFYGDYGGIPTHGVPBMKSKIDPLQARQTYAVGTQHDYFDHDDIIGWTRREGDSS 420
Qy 452 HPNSGLATIMSDGPGGNKMYVGHKAKQVWRDITGNRSGTVTITNADGMNFTVNGAVS 511
Db 421 HPNSGLATIMSDGPGGNKMYVGHKAKQVWRDITGNRSGTVTITNADGMNFTVNGAVS 480
Qy 512 VWVKQ 516
Db 481 VWVKQ 485

RESULT 8
US-08-600-908A-12
Sequence 12, Application US/08600908A
Patent No. 5989169

GENERAL INFORMATION:
APPLICANT: Svendsen, Allan
APPLICANT: Bisg rd-Frantzen, Henrik
APPLICANT: Borchert, Torben Vedel
TITLE OF INVENTION: '-Amylase Mutants
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSER: No. 59891690 No. 5989169disk of No. 5989169th America, Inc.
STREET: 405 Lexington Avenue, 64th Floor
CITY: New York
STATE: New York
COUNTRY: United States of America
ZIP: 10174-6401

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/600,908A
FILING DATE: 13-FEB-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Green, Reza
REGISTRATION NUMBER: 38,475
REFERENCE/DOCKET NUMBER: 4394,204-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 485 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-600-908A-12

Query Match 91.3%; Score 2613; DB 2; Length 485;
Best Local Similarity 95.1%; Pred. No. 3,7e-228;
Matches 461; Conservative 16; Mismatches 8; Indels 0; Gaps 0;

Qy 32 HHNNGTGMQYEFEMHLPNQGNHNRRLDDAANKSKGTTAVWLPAPAKGTSQNDVCGA 91
Db 1 HHNNGTGMQYEFEMHLPNQGNHNRRLDDAANKSKGTTAVWLPAPAKGTSQNDVCGA 60
Qy 92 YDLVLDLSEFNQKGVTRTYGTRSLQAGAVTSLKNGILOYGVVNMHKGADGTEMVAV 151
Db 61 YDLVLDLSEFNQKGVTRTYGTRSLQAGAVTSLKNGILOYGVVNMHKGADGTEMVAV 120
Qy 152 EVNNSNRNOETISGEYTTLEAWTKFDPGKGNTHSNFKRWYHFDGTDMDQSFQLONKIYKF 211
Db 121 EVNNSNRNOETISGEYTTLEAWTKFDPGKGNTHSNFKRWYHFDGTDMDQSFQLONKIYKF 180

Qy 212 RGTGKAMDWEVDIENGNYDILMTADIDMDHPEVINELRNMGWYTNLTNLGDPRIDAVKH 271
Db 181 RGTGKAMDWEVDIENGNYDILMTADIDMDHPEVINELRNMGWYTNLTNLGDPRIDAVKH 240
Qy 272 IKISYTRDMLTHVNTTNGKPEFAVAEFWKNDLAIENYLNKTSWNHSEFVPLHYNLNA 331
Db 241 IKISYTRDMLTHVNTTNGKPEFAVAEFWKNDLAIENYLNKTSWNHSEFVPLHYNLNA 300
Qy 332 SMSGYVPMRNLNGSVVQKPHAVTFVDNHDSPGEBALSFVQWFKPLAVALVLTRE 391
Db 301 SMSGYVPMRNLNGSVVQKPHAVTFVDNHDSPGEBALSFVQWFKPLAVALVLTRE 360
Qy 392 QGYSPVFYGDYGGIPTHGVPBMKSKIDPLQARQTYAVGTQHDYFDHDDIIGWTRREGDSS 451
Db 361 QGYSPVFYGDYGGIPTHGVPBMKSKIDPLQARQTYAVGTQHDYFDHDDIIGWTRREGDSS 420
Qy 452 HPNSGLATIMSDGPGGNKMYVGHKAKQVWRDITGNRSGTVTITNADGMNFTVNGAVS 511
Db 421 HPNSGLATIMSDGPGGNKMYVGHKAKQVWRDITGNRSGTVTITNADGMNFTVNGAVS 480
Qy 512 VWVKQ 516
Db 481 VWVKQ 485

RESULT 9
US-08-683-838A-12
Sequence 12, Application US/08683838A
Patent No. 6022724

GENERAL INFORMATION:
APPLICANT: Svendsen, Allan
APPLICANT: Bisg rd-Frantzen, Henrik
APPLICANT: Borchert, Torben Vedel
TITLE OF INVENTION: '-Amylase Mutants
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSER: No. 60227240 No. 6022724disk of No. 6022724th America, Inc.
STREET: 405 Lexington Avenue, 64th Floor
CITY: New York
STATE: New York
COUNTRY: United States of America
ZIP: 10174-6401

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/683,838A
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/600,908
FILING DATE: 13-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: Green, Reza
REGISTRATION NUMBER: 38,475
REFERENCE/DOCKET NUMBER: 4394,204-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 485 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-683-838A-12

Query Match 91.3%; Score 2613; DB 3; Length 485;
Best Local Similarity 95.1%; Pred. No. 3,7e-228;
Matches 461; Conservative 16; Mismatches 8; Indels 0; Gaps 0;

RESULT 10
 US-08-600-656-1
 Sequence 1, Application US/08600656
 Patent No. 6093562
 GENERAL INFORMATION:
 APPLICANT: Bisgaard-Frantzen, Henrik
 APPLICANT: Svendsen, Allan
 APPLICANT: Borchert, Torben Vedel
 TITLE OF INVENTION: AMYLASE VARIANTS
 NUMBER OF SEQUENCES: 32
 CORRESPONDENCE ADDRESSES:
 ADDRESSEE: No. 60935620 No. 6093562disk of No. 6093562th America, Inc.
 STREET: 405 Lexington Avenue, Suite 6400
 CITY: New York
 STATE: New York
 COUNTRY: U.S.A.
 ZIP: 10174-6401
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent in Release #1.0, Version #1.25 (EPO)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/600,656
 FILING DATE: 13-FEB-1996
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Lambiris, Elias J.
 REGISTRATION NUMBER: 33,728
 REFERENCE/DOCKET NUMBER: 4338.204-US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 212 867 0123
 TELEFAX: 212 867 0298
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 485 amino acids

```
th 485;
els 0; Gaps 0;
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PPAMKGTQNDVGVGA	60
NNHKKGAGDTEMVAV	151
MMHKKGAGDTEIVAV	120
ITDMDQROLOKIKYF	211
ITDMDQROLOKIKYF	180
ITVTLNLDFGRIDAVKH	271
ITVTLNLDFGRIDAVKH	240
INSVDFVPLAHNLVA	331
INSVDFVPLAHNLVA	300
QSMFKPLAYALITRE	391
QOMFKPLAYALITRE	360
PDHHIIIGWTEBGRSS	451
PDHHIIIGWTEBGRSS	420
NADGMGNFTVNGAVS	511
NADGMGNFTVNGAVS	480

ch 485;

Matches 461; Conservative 16; Mismatches 8; Indels 0; Gaps 0;

QY 32 HHNGTNGMMQYFEWHLFNDGNHNRRLDDAANKSKGITAIVWIPPAWKGSQNDVGGA 91
DB 1 HHNGTNGMMQYFEWHLFNDGNHNRRLDDAANKSKGITAIVWIPPAWKGSQNDVGGA 60

QY 92 YDLVDLGEFNQKGVTRTKYGRSLOGAVTSLKNNGIQVGDVVMNHKGADGTEIVNAV 151
DB 61 YDLVDLGEFNQKGVTRTKYGRSLOGAVTSLKNNGIQVGDVVMNHKGADGTEIVNAV 120

QY 152 EVNSNRNOEISGEYTIEMTKPDPGKGNTHSNFKRMWYHFDGTDMDQSRLOKNIYKF 211
DB 121 EVNSNRNOEISGEYTIEMTKPDPGKGNTHSNFKRMWYHFDGTDMDQSRLOKNIYKF 180

QY 212 RGTGKAMDWEVDIENGNDYIMYADIDMDHPEVINELRNMGWYNTNTLNLGFRIDAVKH 271
DB 181 RGTGKAMDWEVDIENGNDYIMYADIDMDHPEVINELRNMGWYNTNTLNLGFRIDAVKH 240

QY 272 IKYSYTRDMLTHVNTTCKPMPFAVAEFWKNDLAAIENYLNKTSNMHSVEFDVPLHYNLYNA 331
DB 241 IKYSYTRDMLTHVNTTCKPMPFAVAEFWKNDLAAIENYLNKTSNMHSVEFDVPLHYNLYNA 300

QY 332 SNSGCVFPMRNIILNGSVVQKPHAVTFVDNHDSPGSALESFVQWFKPLAYALVLTRE 391
DB 301 SNSGCVFPMRNIILNGSVVQKPHAVTFVDNHDSPGSALESFVQWFKPLAYALVLTRE 360

QY 392 QGYSVFYGDYGGIPTHGVPBMKSKIDPLQARQTYAGTQHDYFDHDDIIGMTRREGDS 451
DB 361 QGYSVFYGDYGGIPTHGVPBMKSKIDPLQARQTYAGTQHDYFDHDDIIGMTRREGDS 420

QY 452 HPNSGLATIMSDGPGNKMVYGGKAKAGQVWRDITGNRSGTITINADGNGFTVNGAVS 511
DB 421 HPNSGLATIMSDGPGNKMVYGGKAKAGQVWRDITGNRSGTITINADGNGFTVNGAVS 480

QY 512 VVWVKQ 516
DB 481 VVWVKQ 485

RESULT 12
US-09-170-670-7
; Sequence 7, Application US/09170670
; Patent No. 6187576
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Borchert, Torden
; APPLICANT: Bisgaard-Frantzen, Henrik
; TITLE OF INVENTION: Alpha-Amylase Mutants
; FILE REFERENCE: 5276, 200-US
; CURRENT APPLICATION NUMBER: US/09/170,670
; EARLIER FILING DATE: 1998-10-13
; EARLIER APPLICATION NUMBER: 1172/97
; EARLIER FILING DATE: 1997-10-13
; EARLIER APPLICATION NUMBER: 60/063,306
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 485
; TYPE: PRT
; ORGANISM: Bacillus sp.
US-09-170-670-7

Query Match 91.3%; Score 2613; DB 3; Length 485;
Best Local Similarity 95.1%; Pred. No. 3.7e-228;
Matches 461; Conservative 16; Mismatches 8; Indels 0; Gaps 0;

QY 32 HHNGTNGMMQYFEWHLFNDGNHNRRLDDAANKSKGITAIVWIPPAWKGSQNDVGGA 91
DB 1 HHNGTNGMMQYFEWHLFNDGNHNRRLDDAANKSKGITAIVWIPPAWKGSQNDVGGA 60

QY 92 YDLVDLGEFNQKGVTRTKYGRSLOGAVTSLKNNGIQVGDVVMNHKGADGTEIVNAV 151
DB 61 YDLVDLGEFNQKGVTRTKYGRSLOGAVTSLKNNGIQVGDVVMNHKGADGTEIVNAV 120

QY 152 EVNSNRNOEISGEYTIEMTKPDPGKGNTHSNFKRMWYHFDGTDMDQSRLOKNIYKF 211
DB 121 EVNSNRNOEISGEYTIEMTKPDPGKGNTHSNFKRMWYHFDGTDMDQSRLOKNIYKF 180

QY 212 RGTGKAMDWEVDIENGNDYIMYADIDMDHPEVINELRNMGWYNTNTLNLGFRIDAVKH 271
DB 181 RGTGKAMDWEVDIENGNDYIMYADIDMDHPEVINELRNMGWYNTNTLNLGFRIDAVKH 240

QY 272 IKYSYTRDMLTHVNTTCKPMPFAVAEFWKNDLAAIENYLNKTSNMHSVEFDVPLHYNLYNA 331
DB 241 IKYSYTRDMLTHVNTTCKPMPFAVAEFWKNDLAAIENYLNKTSNMHSVEFDVPLHYNLYNA 300

QY 332 SNSGCVFPMRNIILNGSVVQKPHAVTFVDNHDSPGSALESFVQWFKPLAYALVLTRE 391
DB 301 SNSGCVFPMRNIILNGSVVQKPHAVTFVDNHDSPGSALESFVQWFKPLAYALVLTRE 360

QY 392 QGYSVFYGDYGGIPTHGVPBMKSKIDPLQARQTYAGTQHDYFDHDDIIGMTRREGDS 451
DB 361 QGYSVFYGDYGGIPTHGVPBMKSKIDPLQARQTYAGTQHDYFDHDDIIGMTRREGDS 420

QY 452 HPNSGLATIMSDGPGNKMVYGGKAKAGQVWRDITGNRSGTITINADGNGFTVNGAVS 511
DB 421 HPNSGLATIMSDGPGNKMVYGGKAKAGQVWRDITGNRSGTITINADGNGFTVNGAVS 480

QY 512 VVWVKQ 516
DB 481 VVWVKQ 485

DB 61 YDLVDLGEFNQKGVTRTKYGRSLOGAVTSLKNNGIQVGDVVMNHKGADGTEIVNAV 120

QY 152 EVNSNRNOEISGEYTIEMTKPDPGKGNTHSNFKRMWYHFDGTDMDQSRLOKNIYKF 211
DB 121 EVNSNRNOEISGEYTIEMTKPDPGKGNTHSNFKRMWYHFDGTDMDQSRLOKNIYKF 180

QY 212 RGTGKAMDWEVDIENGNDYIMYADIDMDHPEVINELRNMGWYNTNTLNLGFRIDAVKH 271
DB 181 RGTGKAMDWEVDIENGNDYIMYADIDMDHPEVINELRNMGWYNTNTLNLGFRIDAVKH 240

QY 272 IKYSYTRDMLTHVNTTCKPMPFAVAEFWKNDLAAIENYLNKTSNMHSVEFDVPLHYNLYNA 331
DB 241 IKYSYTRDMLTHVNTTCKPMPFAVAEFWKNDLAAIENYLNKTSNMHSVEFDVPLHYNLYNA 300

QY 332 SNSGCVFPMRNIILNGSVVQKPHAVTFVDNHDSPGSALESFVQWFKPLAYALVLTRE 391
DB 301 SNSGCVFPMRNIILNGSVVQKPHAVTFVDNHDSPGSALESFVQWFKPLAYALVLTRE 360

QY 392 QGYSVFYGDYGGIPTHGVPBMKSKIDPLQARQTYAGTQHDYFDHDDIIGMTRREGDS 451
DB 361 QGYSVFYGDYGGIPTHGVPBMKSKIDPLQARQTYAGTQHDYFDHDDIIGMTRREGDS 420

QY 452 HPNSGLATIMSDGPGNKMVYGGKAKAGQVWRDITGNRSGTITINADGNGFTVNGAVS 511
DB 421 HPNSGLATIMSDGPGNKMVYGGKAKAGQVWRDITGNRSGTITINADGNGFTVNGAVS 480

QY 512 VVWVKQ 516
DB 481 VVWVKQ 485

RESULT 13
US-09-193-068-1
; Sequence 1, Application US/09193068
; Patent No. 6197565
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Kjullf, S ren
; APPLICANT: Bisgaard-Frantzen, Henrik
; TITLE OF INVENTION: -Amylase Variants
; FILE REFERENCE: 5709, 000-US
; CURRENT APPLICATION NUMBER: US/09/193,068
; EARLIER FILING DATE: 1998-11-16
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 485
; TYPE: PRT
; ORGANISM: Bacillus sp.
US-09-193-068-1

Query Match 91.3%; Score 2613; DB 3; Length 485;
Best Local Similarity 95.1%; Pred. No. 3.7e-228;
Matches 461; Conservative 16; Mismatches 8; Indels 0; Gaps 0;

QY 32 HHNGTNGMMQYFEWHLFNDGNHNRRLDDAANKSKGITAIVWIPPAWKGSQNDVGGA 91
DB 1 HHNGTNGMMQYFEWHLFNDGNHNRRLDDAANKSKGITAIVWIPPAWKGSQNDVGGA 60

QY 92 YDLVDLGEFNQKGVTRTKYGRSLOGAVTSLKNNGIQVGDVVMNHKGADGTEIVNAV 151
DB 61 YDLVDLGEFNQKGVTRTKYGRSLOGAVTSLKNNGIQVGDVVMNHKGADGTEIVNAV 120

QY 152 EVNSNRNOEISGEYTIEMTKPDPGKGNTHSNFKRMWYHFDGTDMDQSRLOKNIYKF 211
DB 121 EVNSNRNOEISGEYTIEMTKPDPGKGNTHSNFKRMWYHFDGTDMDQSRLOKNIYKF 180

QY 212 RGTGKAMDWEVDIENGNDYIMYADIDMDHPEVINELRNMGWYNTNTLNLGFRIDAVKH 271
DB 181 RGTGKAMDWEVDIENGNDYIMYADIDMDHPEVINELRNMGWYNTNTLNLGFRIDAVKH 240

QY 272 IKYSYTRDMLTHVNTTCKPMPFAVAEFWKNDLAAIENYLNKTSNMHSVEFDVPLHYNLYNA 331
DB 241 IKYSYTRDMLTHVNTTCKPMPFAVAEFWKNDLAAIENYLNKTSNMHSVEFDVPLHYNLYNA 300

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Db 241 IKTSFTRDMLTHVRNTTGKMPFAVAEFWKNDLGA1ENYLNKTSWNHSPVDFPLHYNLXNA 300
Qy 332 SNSGGYFDMRNIIINGSVVOGHP1HAVTVDNHDSPGEALSFVQSWFKPLAVALITRE 391
Db 301 SNSGGYYDMRNIIINGSVVOGHP1HAVTVDNHDSPGEALSFVQSWFKPLAVALITRE 360
Qy 392 QGYPSVFGDYVGIPTHGVPAMSKIDPLLOARQTAAYGQHDPFHHDITGWTREGDS 451
Db 361 QGYPSVFGDYVGIPTHGVPAMSKIDPLLOARQTFYVGHDPFHHDITGWTREGDS 420
Qy 452 HPSNGIATIMSDPGGNKMMYVGHKAKAGVWRDITGNRSCTVTINADGWNFTVNGAVS 511
Db 421 HPSNGIATIMSDPGGNKMMYVGHKAKAGVWRDITGNRTGTVTINADGWNFTVNGAVS 480
Qy 512 VVWKQ 516
Db 481 VVWKQ 485
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RESULT 14
US-09-193-068-7
; Sequence 7, Application US/09193068
; Patent No. 6197565
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Kjerulff, Soren
; APPLICANT: Bisgaard-Frantzen, Henrik
; APPLICANT: Andersen, Carsten
; TITLE OF INVENTION: -Amylase Variants
; FILE REFERENCE: 5709, 000-US
; CURRENT APPLICATION NUMBER: US/09/193,068
; CURRENT FILING DATE: 1998-11-16
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 485
; TYPE: PR1
; ORGANISM: Bacillus sp.
US-09-193-068-7
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Query Match 91.3%; Score 2613; DB 3; Length 485;
Best Local Similarity 95.1%; Pred. No. 3,7e-228;
Matches 461; Conservative 16; Mismatches 8; Indels 0; Gaps 0;

Qy 32 HNGTNGTMMQYFEMHLPNDGNHNRRLRDAANLKSIGITAVWIIPAMKGTSONDVGYGA 91
Db 1 HNGTNGTMMQYFEMWLPNDGNHNRRLRDAANLKSIGITAVWIIPAMKGTSONDVGYGA 60
Qy 92 YDLYDLGEFNOGKTVTKYGTGTSOLOGAVTSLKNNGIQYVGDVVMNHKGADGTEMVNAV 151
Db 61 YDLYDLGEFNOGKTVTKYGTGTSOLOGAVTSLKNNGIQYVGDVVMNHKGADGTEIYNVAV 120
Qy 152 EVNRSNRNOEISGEYITLAWTKDFPGRGNTSHNFKRWYHFDGTWDSROLONKIYKF 211
Db 121 EVNRSNRNOETSGEYALIAWTKDFPGRGNHSHSFKRWYHFDGTWDSROLONKIYKF 180
Qy 212 RGTGKAMDWEVDIENGNVYDIAMADVMDHPEVYIHELNRMGVWYITNTLINDGFRIDAVKH 271
Db 181 RGTGKAMDWEVDIENGNVYDIAMADVMDHPEVYIHELNRMGVWYITNTLINDGFRIDAVKH 240
Qy 272 IKTSYTRDMLTHVRNTTGKMPFAVAEFWKNDLGA1ENYLNKTSWNHSPVDFPLHYNLXNA 331
Db 241 IKTSFTRDMLTHVRNTTGKMPFAVAEFWKNDLGA1ENYLNKTSWNHSPVDFPLHYNLXNA 300
Qy 332 SNSGGYFDMRNIIINGSVVOGHP1HAVTVDNHDSPGEALSFVQSWFKPLAVALITRE 391
Db 301 SNSGGYYDMRNIIINGSVVOGHP1HAVTVDNHDSPGEALSFVQSWFKPLAVALITRE 360
Qy 392 QGYPSVFGDYVGIPTHGVPAMSKIDPLLOARQTAAYGQHDPFHHDITGWTREGDS 451
Db 361 QGYPSVFGDYVGIPTHGVPAMSKIDPLLOARQTFYVGHDPFHHDITGWTREGDS 420
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Qy 452 HPSNGIATIMSDPGGNKMMYVGHKAKAGVWRDITGNRSCTVTINADGWNFTVNGAVS 511
Db 421 HPSNGIATIMSDPGGNKMMYVGHKAKAGVWRDITGNRTGTVTINADGWNFTVNGAVS 480
Qy 512 VVWKQ 516
Db 481 VVWKQ 485
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RESULT 15
US-09-183-412-1
; Sequence 1, Application US/09183412
; Patent No. 6204232
; GENERAL INFORMATION:
; APPLICANT: Borchert, Torben V.
; APPLICANT: Svendsen, Allan
; APPLICANT: Andersen, Carsten
; APPLICANT: Nielsen, Bjarne
; APPLICANT: Nissen, Torben L.
; APPLICANT: Kjaerulff, Soren
; TITLE OF INVENTION: Alpha-Amylase Mutants
; FILE REFERENCE: 5368, 200-US
; CURRENT APPLICATION NUMBER: US/09/183,412
; CURRENT FILING DATE: 1998-10-30
; EARLIER APPLICATION NUMBER: 60/064,662
; EARLIER FILING DATE: 1997-11-06
; EARLIER APPLICATION NUMBER: 60/093,234
; EARLIER FILING DATE: 1998-07-17
; EARLIER APPLICATION NUMBER: 1240/97
; EARLIER FILING DATE: 1997-10-30
; EARLIER APPLICATION NUMBER: PA 1998 00936
; EARLIER FILING DATE: 1998-07-14
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 485
; TYPE: PR1
; ORGANISM: Bacillus
US-09-183-412-1
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Query Match 91.3%; Score 2613; DB 3; Length 485;
Best Local Similarity 95.1%; Pred. No. 3,7e-228;
Matches 461; Conservative 16; Mismatches 8; Indels 0; Gaps 0;

Qy 32 HNGTNGTMMQYFEMHLPNDGNHNRRLRDAANLKSIGITAVWIIPAMKGTSONDVGYGA 91
Db 1 HNGTNGTMMQYFEMWLPNDGNHNRRLRDAANLKSIGITAVWIIPAMKGTSONDVGYGA 60
Qy 92 YDLYDLGEFNOGKTVTKYGTGTSOLOGAVTSLKNNGIQYVGDVVMNHKGADGTEMVNAV 151
Db 61 YDLYDLGEFNOGKTVTKYGTGTSOLOGAVTSLKNNGIQYVGDVVMNHKGADGTEIYNVAV 120
Qy 152 EVNRSNRNOEISGEYITLAWTKDFPGRGNTSHNFKRWYHFDGTWDSROLONKIYKF 211
Db 121 EVNRSNRNOETSGEYALIAWTKDFPGRGNHSHSFKRWYHFDGTWDSROLONKIYKF 180
Qy 212 RGTGKAMDWEVDIENGNVYDIAMADVMDHPEVYIHELNRMGVWYITNTLINDGFRIDAVKH 271
Db 181 RGTGKAMDWEVDIENGNVYDIAMADVMDHPEVYIHELNRMGVWYITNTLINDGFRIDAVKH 240
Qy 272 IKTSYTRDMLTHVRNTTGKMPFAVAEFWKNDLGA1ENYLNKTSWNHSPVDFPLHYNLXNA 331
Db 241 IKTSFTRDMLTHVRNTTGKMPFAVAEFWKNDLGA1ENYLNKTSWNHSPVDFPLHYNLXNA 300
Qy 332 SNSGGYFDMRNIIINGSVVOGHP1HAVTVDNHDSPGEALSFVQSWFKPLAVALITRE 391
Db 301 SNSGGYYDMRNIIINGSVVOGHP1HAVTVDNHDSPGEALSFVQSWFKPLAVALITRE 360
Qy 392 QGYPSVFGDYVGIPTHGVPAMSKIDPLLOARQTAAYGQHDPFHHDITGWTREGDS 451
Db 361 QGYPSVFGDYVGIPTHGVPAMSKIDPLLOARQTFYVGHDPFHHDITGWTREGDS 420
Qy 452 HPSNGIATIMSDPGGNKMMYVGHKAKAGVWRDITGNRSCTVTINADGWNFTVNGAVS 511
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Db 421 HPNSGLATIMSDPGGNKMTYVGNKAKGVWRDITGNRTGTITVADGMGNFSVNGSSVS 480

OY 512 VVWKO 516

Db 481 VVWKO 485

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Job time : 26 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

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(without alignments)
2817.750 Million cell updates/sec

Title: US-08-952-741-2
Perfect score: 2862
Sequence: 1 MKNLRRIISVLTLLAVAV.....ADGNGNFTNGAVSVWVKQ 516

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

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Total number of hits satisfying chosen parameters: 1426032

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	2862	100.0	516	US-09-971-611-2	Sequence 2, Appli
3	2862	100.0	516	US-10-399-161-8	Sequence 8, Appli
4	2613	91.3	485	US-09-769-864-1	Sequence 1, Appli
5	2613	91.3	485	US-09-769-864-7	Sequence 7, Appli
6	2613	91.3	485	US-09-854-346-2	Sequence 2, Appli
7	2613	91.3	485	US-09-902-188A-1	Sequence 1, Appli
8	2613	91.3	485	US-09-918-543-2	Sequence 2, Appli
9	2613	91.3	485	US-09-795-211-1	Sequence 1, Appli
10	2613	91.3	485	US-09-925-576C-2	Sequence 2, Appli
11	2613	91.3	485	US-10-025-648-1	Sequence 1, Appli
12	2613	91.3	485	US-10-184-771-12	Sequence 12, Appli
13	2613	91.3	485	US-10-327-837-1	Sequence 1, Appli

14	2613	91.3	485	US-10-327-837-7	Sequence 7, Appli
15	2613	91.3	485	US-10-665-667-1	Sequence 1, Appli
16	2613	91.3	485	US-10-665-667-7	Sequence 7, Appli
17	2613	91.3	485	US-10-477-725-2	Sequence 2, Appli
18	2613	91.3	485	US-10-926-720-12	Sequence 12, Appli
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21	2613	91.3	485	US-10-980-923-7	Sequence 7, Appli
22	2466.5	86.2	516	US-10-343-212-2	Sequence 2, Appli
23	2440	85.3	485	US-09-769-864-2	Sequence 2, Appli
24	2440	85.3	485	US-09-769-864-8	Sequence 8, Appli
25	2440	85.3	485	US-09-854-346-4	Sequence 4, Appli
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27	2440	85.3	485	US-09-918-543-1	Sequence 1, Appli
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41	2410	84.2	485	US-09-902-188A-7	Sequence 7, Appli
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43	2410	84.2	485	US-10-025-648-7	Sequence 7, Appli
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45	2410	84.2	485	US-10-665-667-6	Sequence 6, Appli

ALIGNMENTS

RESULT 1
US-09-986-676A-2
Sequence 2, Application US/09986676A
Patent No. US20020102698A1
GENERAL INFORMATION:
APPLICANT: HATADA, Yoji
APPLICANT: OZAKI, Katsuya
APPLICANT: ARA, Katsutoshi
APPLICANT: KAWAI, Shuji
APPLICANT: ITO, Susumu
TITLE OF INVENTION: Gene Encoding Alkaline Liquefying Alpha-Amylase
FILE REFERENCE: 2173-0121P
CURRENT APPLICATION NUMBER: US/09/986,676A
CURRENT FILING DATE: 2001-11-09
PRIOR APPLICATION NUMBER: PCT/JP96/01641
PRIOR FILING DATE: 1996-06-14
PRIOR APPLICATION NUMBER: Japan 147257/1995
PRIOR FILING DATE: 1995-06-14
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2
LENGTH: 516
TYPE: PRT
ORGANISM: Bacillus sp.
US-09-986-676A-2
Query Match 100.0%; Score 2862; DB 9; Length 516;
Best Local Similarity 100.0%; Pred. No. 2, 7e-239;
Matches 516; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 61 DAANLKSKITAVWIPPAKGTSONDVGYGAYDYLDELGFNOKGIVRTKYGTRSQLQAV 120
QY 121 TSLKNNGIQVYGVVNNHKGADGTEMVNAVEVNRNNOEISGEYTIEMTKFDPGRG 180
Db 121 TSLKNNGIQVYGVVNNHKGADGTEMVNAVEVNRNNOEISGEYTIEMTKFDPGRG 180
QY 181 NTHSNFKMRYHFDGTDMDQSRLOKIKYFRGTGAMWEDVIEENGNDYLMYADIDMD 240
Db 181 NTHSNFKMRYHFDGTDMDQSRLOKIKYFRGTGAMWEDVIEENGNDYLMYADIDMD 240
QY 241 HPEVINELNMGWYNTNLNDGFRIDAVKHIKYSTYRDMLTFRVNTTGKPMFAVAEFWK 300
Db 241 HPEVINELNMGWYNTNLNDGFRIDAVKHIKYSTYRDMLTFRVNTTGKPMFAVAEFWK 300
QY 301 NDLAALIENTLNTKSNHSAFVDFPLAHYNLYNASNSGGYFPMRNILNLSVVOKPIHAATFV 360
Db 301 NDLAALIENTLNTKSNHSAFVDFPLAHYNLYNASNSGGYFPMRNILNLSVVOKPIHAATFV 360
QY 361 DNHDSPGEGALBSFVOSWFKPLAYALILTRGOYPSVFYGDYGIPTHGVPMSKSIDPL 420
Db 361 DNHDSPGEGALBSFVOSWFKPLAYALILTRGOYPSVFYGDYGIPTHGVPMSKSIDPL 420
QY 421 LQARQTYAYGTQHDYDFDHDIIIGWTRBGDSHPNSGLATIMSDPGGNKMYVGGKHAQ 480
Db 421 LQARQTYAYGTQHDYDFDHDIIIGWTRBGDSHPNSGLATIMSDPGGNKMYVGGKHAQ 480
QY 481 VNRDITGNRSQVITINADGNGFTVNGAVSVWVKQ 516
Db 481 VNRDITGNRSQVITINADGNGFTVNGAVSVWVKQ 516

RESULT 2
US-09-971-611-2
; Sequence 2, Application US/09971611
; Patent No. US20020123124A1
; GENERAL INFORMATION:
; APPLICANT: ARAKI, HIROYUKI
; APPLICANT: ENDO, KEIJI
; APPLICANT: HAGIHARA, HIROSHI
; APPLICANT: IGARASHI, KAZUAKI
; APPLICANT: HAYASHI, YASUHIRO
; APPLICANT: OZAKI, KATSUYA
; TITLE OF INVENTION: HIGHLY PRODUCTIVE ALPHA-AMYLASES
; FILE REFERENCE: 214377US0
; CURRENT APPLICATION NUMBER: US/09/971,611
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: JP 2000/310605
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 2
; LENGTH: 516
; TYPE: PRN
; ORGANISM: Bacillus sp. KSM-Ap1378
; US-09-971-611-2

Query Match 100.0%; Score 2862; DB 9; Length 516;
Best Local Similarity 100.0%; Pred. No. 2,7e-239;
Matches 516; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MKLHNRILISVLLTLLAVAVLPFYMTPEAOAHNNGTGMQYFEWHLPRNDGNHNRRLD 60
Db 1 MKLHNRILISVLLTLLAVAVLPFYMTPEAOAHNNGTGMQYFEWHLPRNDGNHNRRLD 60
QY 61 DAANLKSKITAVWIPPAKGTSONDVGYGAYDYLDELGFNOKGIVRTKYGTRSQLQAV 120
Db 61 DAANLKSKITAVWIPPAKGTSONDVGYGAYDYLDELGFNOKGIVRTKYGTRSQLQAV 120
QY 121 TSLKNNGIQVYGVVNNHKGADGTEMVNAVEVNRNNOEISGEYTIEMTKFDPGRG 180
Db 121 TSLKNNGIQVYGVVNNHKGADGTEMVNAVEVNRNNOEISGEYTIEMTKFDPGRG 180
QY 181 NTHSNFKMRYHFDGTDMDQSRLOKIKYFRGTGAMWEDVIEENGNDYLMYADIDMD 240
Db 181 NTHSNFKMRYHFDGTDMDQSRLOKIKYFRGTGAMWEDVIEENGNDYLMYADIDMD 240

Db 181 NTHSNFKMRYHFDGTDMDQSRLOKIKYFRGTGAMWEDVIEENGNDYLMYADIDMD 240
QY 241 HPEVINELNMGWYNTNLNDGFRIDAVKHIKYSTYRDMLTFRVNTTGKPMFAVAEFWK 300
Db 241 HPEVINELNMGWYNTNLNDGFRIDAVKHIKYSTYRDMLTFRVNTTGKPMFAVAEFWK 300
QY 301 NDLAALIENTLNTKSNHSAFVDFPLAHYNLYNASNSGGYFPMRNILNLSVVOKPIHAATFV 360
Db 301 NDLAALIENTLNTKSNHSAFVDFPLAHYNLYNASNSGGYFPMRNILNLSVVOKPIHAATFV 360
QY 361 DNHDSPGEGALBSFVOSWFKPLAYALILTRGOYPSVFYGDYGIPTHGVPMSKSIDPL 420
Db 361 DNHDSPGEGALBSFVOSWFKPLAYALILTRGOYPSVFYGDYGIPTHGVPMSKSIDPL 420
QY 421 LQARQTYAYGTQHDYDFDHDIIIGWTRBGDSHPNSGLATIMSDPGGNKMYVGGKHAQ 480
Db 421 LQARQTYAYGTQHDYDFDHDIIIGWTRBGDSHPNSGLATIMSDPGGNKMYVGGKHAQ 480
QY 481 VNRDITGNRSQVITINADGNGFTVNGAVSVWVKQ 516
Db 481 VNRDITGNRSQVITINADGNGFTVNGAVSVWVKQ 516

RESULT 3
US-10-399-161-8
; Sequence 8, Application US/10399161
; Publication No. US20040091994A1
; GENERAL INFORMATION:
; APPLICANT: Andersen, Carsten
; TITLE OF INVENTION: Alpha-amylase variant with altered properties
; FILE REFERENCE: 10115, 204-WO
; CURRENT APPLICATION NUMBER: US/10/399,161
; PRIOR FILING DATE: 2003-04-11
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 8
; LENGTH: 516
; TYPE: PRN
; ORGANISM: Bacillus sp.
; US-10-399-161-8

Query Match 100.0%; Score 2862; DB 15; Length 516;
Best Local Similarity 100.0%; Pred. No. 2,7e-239;
Matches 516; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MKLHNRILISVLLTLLAVAVLPFYMTPEAOAHNNGTGMQYFEWHLPRNDGNHNRRLD 60
Db 1 MKLHNRILISVLLTLLAVAVLPFYMTPEAOAHNNGTGMQYFEWHLPRNDGNHNRRLD 60
QY 61 DAANLKSKITAVWIPPAKGTSONDVGYGAYDYLDELGFNOKGIVRTKYGTRSQLQAV 120
Db 61 DAANLKSKITAVWIPPAKGTSONDVGYGAYDYLDELGFNOKGIVRTKYGTRSQLQAV 120
QY 121 TSLKNNGIQVYGVVNNHKGADGTEMVNAVEVNRNNOEISGEYTIEMTKFDPGRG 180
Db 121 TSLKNNGIQVYGVVNNHKGADGTEMVNAVEVNRNNOEISGEYTIEMTKFDPGRG 180
QY 181 NTHSNFKMRYHFDGTDMDQSRLOKIKYFRGTGAMWEDVIEENGNDYLMYADIDMD 240
Db 181 NTHSNFKMRYHFDGTDMDQSRLOKIKYFRGTGAMWEDVIEENGNDYLMYADIDMD 240
QY 241 HPEVINELNMGWYNTNLNDGFRIDAVKHIKYSTYRDMLTFRVNTTGKPMFAVAEFWK 300
Db 241 HPEVINELNMGWYNTNLNDGFRIDAVKHIKYSTYRDMLTFRVNTTGKPMFAVAEFWK 300
QY 301 NDLAALIENTLNTKSNHSAFVDFPLAHYNLYNASNSGGYFPMRNILNLSVVOKPIHAATFV 360
Db 301 NDLAALIENTLNTKSNHSAFVDFPLAHYNLYNASNSGGYFPMRNILNLSVVOKPIHAATFV 360
QY 361 DNHDSPGEGALBSFVOSWFKPLAYALILTRGOYPSVFYGDYGIPTHGVPMSKSIDPL 420
Db 361 DNHDSPGEGALBSFVOSWFKPLAYALILTRGOYPSVFYGDYGIPTHGVPMSKSIDPL 420

Qy 421 LOARQYAVGTQHDYFDHHDIGWTRBDSHPNSGLATIMSDPGGKMMYVGKHAGQ 480
Db 421 LOARQYAVGTQHDYFDHHDIGWTRBDSHPNSGLATIMSDPGGKMMYVGKHAGQ 480
Qy 481 VWRDITGNRSQGVITINADGWNFTVNGGAVSVWVKQ 516
Db 481 VWRDITGNRSQGVITINADGWNFTVNGGAVSVWVKQ 516

RESULT 4
US-09-769-864-1
; Sequence 1, Application US/09769864
; Patent No. US20010039253A1
; GENERAL INFORMATION:

; APPLICANT: Borchert, Torben V.
; APPLICANT: Svendsen, Allan
; APPLICANT: Andersen, Carsten
; APPLICANT: Nielsen, Bjarne
; APPLICANT: Nielsen, Torben L.
; APPLICANT: Kjaerulff, Soren
; TITLE OF INVENTION: Alpha-Amylase Mutants
; FILE REFERENCE: 5368.200-US
; CURRENT APPLICATION NUMBER: US/09/769,864
; CURRENT FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 09/183,412
; PRIOR FILING DATE: 1998-10-30
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 485
; TYPE: PR
; ORGANISM: Bacillus
US-09-769-864-1

Query Match 91.3%; Score 2613; DB 9; Length 485;
Best Local Similarity 95.1%; Pred. No. 9.7e-218;
Matches 461; Conservative 16; Mismatches 8; Indels 0; Gaps 0;

Qy 32 HHNGTNGTMMQYFPMHLPNDGNHNRRLDDAANKSGITAVWIPPMWKGTSQNDVGYGA 91
Db 1 HHNGTNGTMMQYFPMHLPNDGNHNRRLDDAANKSGITAVWIPPMWKGTSQNDVGYGA 60
Qy 92 YDLVDLSEFNQKGVTRKYGTRNOLAAYTSLKNGIQQVGDVYMNHKGADGTEIMNAV 151
Db 61 YDLVDLSEFNQKGVTRKYGTRNOLAAYTSLKNGIQQVGDVYMNHKGADGTEIMNAV 120
Qy 152 EVNRSNNOEISGEYTIEMTKFDPGRCNTHSNFKRWYHFDGTDMDQSRQONKIYKF 211
Db 121 EVNRSNNOEISGEYTIEMTKFDPGRCNTHSNFKRWYHFDGTDMDQSRQONKIYKF 180
Qy 212 RGCGKAMDWEVDLENGYDYIMADIMDHEVINELRNNGVWYTNLTINDGFRIDA VKH 271
Db 181 RGCGKAMDWEVDLENGYDYIMADIMDHEVINELRNNGVWYTNLTINDGFRIDA VKH 240
Qy 272 IKSYTRDMLTHVRNTGKEMPAFAEFWKNDLAIENYLNKTSWNHVSFVDPPLHYNL YNA 331
Db 241 IKSYTRDMLTHVRNTGKEMPAFAEFWKNDLAIENYLNKTSWNHVSFVDPPLHYNL YNA 300
Qy 332 SNSGGYEDMNIILNGSVVQKHPIHAVT FVNDHDSQPEALESFVQWFKPLAVALILTRE 391
Db 301 SNSGGYEDMNIILNGSVVQKHPIHAVT FVNDHDSQPEALESFVQWFKPLAVALILTRE 360
Qy 392 QGIPSVFYGYIGYIPTHGVPSMKSIDPLLOARQTYAVGTQHDYFDHHDIIIGWTRBDS 451
Db 361 QGIPSVFYGYIGYIPTHGVPSMKSIDPLLOARQTYAVGTQHDYFDHHDIIIGWTRBDS 420
Qy 452 HPNSGLATIMSDPGGKMMYVGKHAGQVWRDITGNRSQGVITINADGWNFTVNGGAVS 511
Db 421 HPNSGLATIMSDPGGKMMYVGKHAGQVWRDITGNRSQGVITINADGWNFTVNGGAVS 480
Qy 512 VWVKQ 516
Db 512 VWVKQ 516

Db 481 VWVKQ 485

RESULT 5
US-09-769-864-7
; Sequence 7, Application US/09769864
; Patent No. US20010039253A1
; GENERAL INFORMATION:

; APPLICANT: Borchert, Torben V.
; APPLICANT: Svendsen, Allan
; APPLICANT: Andersen, Carsten
; APPLICANT: Nielsen, Bjarne
; APPLICANT: Nielsen, Torben L.
; APPLICANT: Kjaerulff, Soren
; TITLE OF INVENTION: Alpha-Amylase Mutants
; FILE REFERENCE: 5368.200-US
; CURRENT APPLICATION NUMBER: US/09/769,864
; CURRENT FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 09/183,412
; PRIOR FILING DATE: 1998-10-30
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 485
; TYPE: PR
; ORGANISM: Bacillus sp.
US-09-769-864-7

Query Match 91.3%; Score 2613; DB 9; Length 485;
Best Local Similarity 95.1%; Pred. No. 9.7e-218;
Matches 461; Conservative 16; Mismatches 8; Indels 0; Gaps 0;

Qy 32 HHNGTNGTMMQYFPMHLPNDGNHNRRLDDAANKSGITAVWIPPMWKGTSQNDVGYGA 91
Db 1 HHNGTNGTMMQYFPMHLPNDGNHNRRLDDAANKSGITAVWIPPMWKGTSQNDVGYGA 60
Qy 92 YDLVDLSEFNQKGVTRKYGTRNOLAAYTSLKNGIQQVGDVYMNHKGADGTEIMNAV 151
Db 61 YDLVDLSEFNQKGVTRKYGTRNOLAAYTSLKNGIQQVGDVYMNHKGADGTEIMNAV 120
Qy 152 EVNRSNNOEISGEYTIEMTKFDPGRCNTHSNFKRWYHFDGTDMDQSRQONKIYKF 211
Db 121 EVNRSNNOEISGEYTIEMTKFDPGRCNTHSNFKRWYHFDGTDMDQSRQONKIYKF 180
Qy 212 RGCGKAMDWEVDLENGYDYIMADIMDHEVINELRNNGVWYTNLTINDGFRIDA VKH 271
Db 181 RGCGKAMDWEVDLENGYDYIMADIMDHEVINELRNNGVWYTNLTINDGFRIDA VKH 240
Qy 272 IKSYTRDMLTHVRNTGKEMPAFAEFWKNDLAIENYLNKTSWNHVSFVDPPLHYNL YNA 331
Db 241 IKSYTRDMLTHVRNTGKEMPAFAEFWKNDLAIENYLNKTSWNHVSFVDPPLHYNL YNA 300
Qy 332 SNSGGYEDMNIILNGSVVQKHPIHAVT FVNDHDSQPEALESFVQWFKPLAVALILTRE 391
Db 301 SNSGGYEDMNIILNGSVVQKHPIHAVT FVNDHDSQPEALESFVQWFKPLAVALILTRE 360
Qy 392 QGIPSVFYGYIGYIPTHGVPSMKSIDPLLOARQTYAVGTQHDYFDHHDIIIGWTRBDS 451
Db 361 QGIPSVFYGYIGYIPTHGVPSMKSIDPLLOARQTYAVGTQHDYFDHHDIIIGWTRBDS 420
Qy 452 HPNSGLATIMSDPGGKMMYVGKHAGQVWRDITGNRSQGVITINADGWNFTVNGGAVS 511
Db 421 HPNSGLATIMSDPGGKMMYVGKHAGQVWRDITGNRSQGVITINADGWNFTVNGGAVS 480
Qy 512 VWVKQ 516
Db 481 VWVKQ 485

RESULT 6
US-09-854-346-2
; Sequence 2, Application US/09854346
; Patent No. US20020068352A1

GENERAL INFORMATION:
 APPLICANT: No. US20020068352A1ozymes A/S
 APPLICANT: Svendsen, Allan
 APPLICANT: Jorgensen, Christel Thea
 APPLICANT: Nielsen, Bjarne Ronfeldt
 FILE OF INVENTION: Alpha-amylase variants with altered 1,6 activity
 CURRENT APPLICATION NUMBER: US/09/854,346
 CURRENT FILING DATE: 2001-05-11
 NUMBER OF SEQ ID NOS: 15
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO: 2
 LENGTH: 485
 TYPE: PRT
 ORGANISM: Bacillus sp.
 US-09-854-346-2

Query Match 91.3%; Score 2613; DB 9; Length 485;
 Best Local Similarity 95.1%; Pred. No. 9.7e-218;
 Matches 461; Conservative 16; Mismatches 8; Indels 0; Gaps 0;

32 HNGTNGTMMQYFEWMLPNDGNHMRRLRDAANLKSKITAVWIPAMKGTSONDVGYGA 91
 1 HNGTNGTMMQYFEWMLPNDGNHMRRLRDAANLKSKITAVWIPAMKGTSONDVGYGA 60
 92 YDIYDGEFNQKGTVRTKGTGTSQLOGAVTSLKNGIOYVGVVNMHKGAGDGTENVNAV 151
 61 YDIYDGEFNQKGTVRTKGTGTSQLOGAVTSLKNGIOYVGVVNMHKGAGDGTENVNAV 120
 152 EVNRSNRNOISGEYTIEMTKFDPGRGNTSHNFKRWYHFDGTDMDOSROLONKIYKF 211
 121 EVNRSNRNOISGEYTIEMTKFDPGRGNTSHNFKRWYHFDGTDMDOSROLONKIYKF 180
 212 RGTGKADWEVDIENGNYDYLMTADIDMDPEVINELRWGWYTYTTLNDGFRIDAVKH 271
 181 RGTGKADWEVDIENGNYDYLMTADIDMDPEVINELRWGWYTYTTLNDGFRIDAVKH 240
 272 IKSYTRDMTLTHRNTTGKPMFAVAEFKNDLAIENYLNKTSWNHSEVDFVPLHYLYNA 331
 241 IKSYTRDMTLTHRNTTGKPMFAVAEFKNDLAIENYLNKTSWNHSEVDFVPLHYLYNA 300
 332 SMSGYFDMNINLNGSVVQKPHIAVTFVNDHDSQGEALLESFVQSFKPLAVALITRE 391
 301 SMSGYFDMNINLNGSVVQKPHIAVTFVNDHDSQGEALLESFVQSFKPLAVALITRE 360
 392 QGYPSVFGDYGIPTHGVPMSKSIDPLLOAQRTYAYGTQHDYFDHDIIGWTRGDS 451
 361 QGYPSVFGDYGIPTHGVPMSKSIDPLLOAQRTYAYGTQHDYFDHDIIGWTRGDS 420
 452 HPNSGLATIMSDGPGKMKMYVGHKAGOWARDITGNRSQVTITNADGNGFTVNGGAVS 511
 421 HPNSGLATIMSDGPGKMKMYVGHKAGOWARDITGNRSQVTITNADGNGFTVNGGAVS 480
 512 VWYKQ 516
 481 VWYKQ 485

RESULT 7
 US-09-902-188A-1
 Sequence 1, Application US/09902188A
 Patent No. US2002009896A1
 GENERAL INFORMATION:
 APPLICANT: Bisgaard-Frantzen, Henrik
 Svendsen, Allan
 Borchert, Torben Vedel
 TITLE OF INVENTION: AMYLASE VARIANTS
 NUMBER OF SEQUENCES: 32
 CORRESPONDENCE ADDRESS:
 ADDRESSSEE: No. US2002009896A1o No. US2002009896A1disk of No. US200200985
 STREET: 405 Lexington Avenue, Suite 6400
 CITY: New York
 STATE: New York

COUNTRY: U.S.A.
 ZIP: 10174-6401
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/902,188A
 FILING DATE: 10-Jan-2001
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 09/354,191
 FILING DATE: <Unknown>
 ATTORNEY/AGENT INFORMATION:
 NAME: Lambitis, Elias J.
 REGISTRATION NUMBER: 33,728
 REFERENCE/DOCKET NUMBER: 4318.204-US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 212 867 0123
 TELEFAX: 212 867 0298
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 485 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 SEQUENCE DESCRIPTION: SEQ ID NO: 1:
 US-09-902-188A-1

Query Match 91.3%; Score 2613; DB 9; Length 485;
 Best Local Similarity 95.1%; Pred. No. 9.7e-218;
 Matches 461; Conservative 16; Mismatches 8; Indels 0; Gaps 0;

32 HNGTNGTMMQYFEWMLPNDGNHMRRLRDAANLKSKITAVWIPAMKGTSONDVGYGA 91
 1 HNGTNGTMMQYFEWMLPNDGNHMRRLRDAANLKSKITAVWIPAMKGTSONDVGYGA 60
 92 YDIYDGEFNQKGTVRTKGTGTSQLOGAVTSLKNGIOYVGVVNMHKGAGDGTENVNAV 151
 61 YDIYDGEFNQKGTVRTKGTGTSQLOGAVTSLKNGIOYVGVVNMHKGAGDGTENVNAV 120
 152 EVNRSNRNOISGEYTIEMTKFDPGRGNTSHNFKRWYHFDGTDMDOSROLONKIYKF 211
 121 EVNRSNRNOISGEYTIEMTKFDPGRGNTSHNFKRWYHFDGTDMDOSROLONKIYKF 180
 212 RGTGKADWEVDIENGNYDYLMTADIDMDPEVINELRWGWYTYTTLNDGFRIDAVKH 271
 181 RGTGKADWEVDIENGNYDYLMTADIDMDPEVINELRWGWYTYTTLNDGFRIDAVKH 240
 272 IKSYTRDMTLTHRNTTGKPMFAVAEFKNDLAIENYLNKTSWNHSEVDFVPLHYLYNA 331
 241 IKSYTRDMTLTHRNTTGKPMFAVAEFKNDLAIENYLNKTSWNHSEVDFVPLHYLYNA 300
 332 SMSGYFDMNINLNGSVVQKPHIAVTFVNDHDSQGEALLESFVQSFKPLAVALITRE 391
 301 SMSGYFDMNINLNGSVVQKPHIAVTFVNDHDSQGEALLESFVQSFKPLAVALITRE 360
 392 QGYPSVFGDYGIPTHGVPMSKSIDPLLOAQRTYAYGTQHDYFDHDIIGWTRGDS 451
 361 QGYPSVFGDYGIPTHGVPMSKSIDPLLOAQRTYAYGTQHDYFDHDIIGWTRGDS 420
 452 HPNSGLATIMSDGPGKMKMYVGHKAGOWARDITGNRSQVTITNADGNGFTVNGGAVS 511
 421 HPNSGLATIMSDGPGKMKMYVGHKAGOWARDITGNRSQVTITNADGNGFTVNGGAVS 480
 512 VWYKQ 516
 481 VWYKQ 485

RESULT 8

US-09-918-543-2
 ; Sequence 2, Application US/09918543
 ; Patent No. US20020155574A1
 ; GENERAL INFORMATION:
 ; APPLICANT: No. US20020155574A1ozymes A/S
 ; APPLICANT: Thisted, Thomas
 ; APPLICANT: Kjaerulf, Soren
 ; APPLICANT: Andersen, Carsten
 ; APPLICANT: Fuglaang, Claus Crone
 ; TITLE OF INVENTION: Alpha-amylase mutants with altered properties
 ; FILE REFERENCE: 10062.200-US
 ; CURRENT APPLICATION NUMBER: US/09/918,543
 ; CURRENT FILING DATE: 2001-07-31
 ; NUMBER OF SEQ ID NOS: 30
 ; SOFTWARE: Patentin version 3.1
 ; SEQ ID NO 2
 ; LENGTH: 485
 ; TYPE: PRT
 ; ORGANISM: Bacillus sp.
 ; US-09-918-543-2

Query Match 91.3%; Score 2613; DB 9; Length 485;
 Best Local Similarity 95.1%; Pred. No. 9.7e-218;
 Matches 461; Conservative 16; Mismatches 8; Indels 0; Gaps 0;

Qy 32 HHNGTNGTMMQYFEMHLPNDGNHNRRLRDAANLKSIGITAVWI.PPAWKGTSQNDVGGA 91
 Db 1 HHNGTNGTMMQYFEMHLPNDGNHNRRLRDAANLKSIGITAVWI.PPAWKGTSQNDVGGA 60
 Qy 92 YDLVDLGEFNOKGIVRTKYGTGRSLOGAVTSLKNGGIQVYGDVVMNHKGADGTEMVNAV 151
 Db 61 YDLVDLGEFNOKGIVRTKYGTGRNLOQAATSLKNGGIQVYGDVVMNHKGADGTEIYNVAV 120
 Qy 152 EVNRSNRNOEISGEYTTIEMTKFDPGKGNTHSNFKRWYHFDGTDWDQSRLODKIYKF 211
 Db 121 EVNRSNRNOEISGEYTTIEMTKFDPGKGNTHSNFKRWYHFDGTDWDQSRLODKIYKF 180
 Qy 212 RGGKADMEVDINGNVDIYMDVMDHDEVLNELRNMGVWYTNLTNLDFRIDAVKH 271
 Db 181 RGTAKADMEVDINGNVDIYMDVMDHDEVLNELRNMGVWYTNLTNLDFRIDAVKH 240
 Qy 272 IKYSYTRDMLTHVANTTGKPMFAVAEFKNDLAAIENYLNKTSNNHSHVDFVPLHYNLXNA 331
 Db 241 IKYSYTRDMLTHVANTTGKPMFAVAEFKNDLAAIENYLNKTSNNHSHVDFVPLHYNLXNA 300
 Qy 332 SNSGGYEDMRNINLNGSVYQKPIHAAVTFVNDHDSQPEALESFYQWFKPLAVALILTRE 391
 Db 301 SNSGGYEDMRNINLNGSVYQKPIHAAVTFVNDHDSQPEALESFYQWFKPLAVALILTRE 360
 Qy 392 QGYPSVRYGYYGIPTHGVPSMKSKIDPLQAROTYAVGTQHDYFDHDDIIGWTRBGSS 451
 Db 361 QGYPSVRYGYYGIPTHGVPSMKSKIDPLQAROTYAVGTQHDYFDHDDIIGWTRBGSS 420
 Qy 452 HPNSGLATIMSDBGKMKMYVGGKAKAGVWRDITGNRSYVTITNADGKGFVNGGAVS 511
 Db 421 HPNSGLATIMSDBGKMKMYVGGKAKAGVWRDITGNRSYVTITNADGKGFVNGGAVS 480
 Qy 512 VVWVQ 516
 Db 481 VVWVQ 485

RESULT 9
 US-09-795-211-1
 ; Sequence 1, Application US/09795211
 ; Publication No. US20020183226A1
 ; GENERAL INFORMATION:
 ; APPLICANT: The Procter & Gamble Company
 ; APPLICANT: Kaesturi, Chandrika
 ; APPLICANT: Wandestrat, Mark E.
 ; APPLICANT: Song, Brian X.
 ; TITLE OF INVENTION: LIQUID DETERGENT COMPOSITION EXHIBITING ENHANCED a-AMYLASE ENZYME
 ; TITLE OF INVENTION: STABILITY

FILE REFERENCE: Detergent Composition
 ; CURRENT APPLICATION NUMBER: US/09/795,211
 ; CURRENT FILING DATE: 2001-02-28
 ; NUMBER OF SEQ ID NOS: 4
 ; SOFTWARE: Patentin version 3.1
 ; SEQ ID NO 1
 ; LENGTH: 485
 ; TYPE: PRT
 ; ORGANISM: alkaliphilicbacillus
 ; US-09-795-211-1

Query Match 91.3%; Score 2613; DB 9; Length 485;
 Best Local Similarity 95.1%; Pred. No. 9.7e-218;
 Matches 461; Conservative 16; Mismatches 8; Indels 0; Gaps 0;

Qy 32 HHNGTNGTMMQYFEMHLPNDGNHNRRLRDAANLKSIGITAVWI.PPAWKGTSQNDVGGA 91
 Db 1 HHNGTNGTMMQYFEMHLPNDGNHNRRLRDAANLKSIGITAVWI.PPAWKGTSQNDVGGA 60
 Qy 92 YDLVDLGEFNOKGIVRTKYGTGRSLOGAVTSLKNGGIQVYGDVVMNHKGADGTEMVNAV 151
 Db 61 YDLVDLGEFNOKGIVRTKYGTGRNLOQAATSLKNGGIQVYGDVVMNHKGADGTEIYNVAV 120
 Qy 152 EVNRSNRNOEISGEYTTIEMTKFDPGKGNTHSNFKRWYHFDGTDWDQSRLODKIYKF 211
 Db 121 EVNRSNRNOEISGEYTTIEMTKFDPGKGNTHSNFKRWYHFDGTDWDQSRLODKIYKF 180
 Qy 212 RGGKADMEVDINGNVDIYMDVMDHDEVLNELRNMGVWYTNLTNLDFRIDAVKH 271
 Db 181 RGTAKADMEVDINGNVDIYMDVMDHDEVLNELRNMGVWYTNLTNLDFRIDAVKH 240
 Qy 272 IKYSYTRDMLTHVANTTGKPMFAVAEFKNDLAAIENYLNKTSNNHSHVDFVPLHYNLXNA 331
 Db 241 IKYSYTRDMLTHVANTTGKPMFAVAEFKNDLAAIENYLNKTSNNHSHVDFVPLHYNLXNA 300
 Qy 332 SNSGGYEDMRNINLNGSVYQKPIHAAVTFVNDHDSQPEALESFYQWFKPLAVALILTRE 391
 Db 301 SNSGGYEDMRNINLNGSVYQKPIHAAVTFVNDHDSQPEALESFYQWFKPLAVALILTRE 360
 Qy 392 QGYPSVRYGYYGIPTHGVPSMKSKIDPLQAROTYAVGTQHDYFDHDDIIGWTRBGSS 451
 Db 361 QGYPSVRYGYYGIPTHGVPSMKSKIDPLQAROTYAVGTQHDYFDHDDIIGWTRBGSS 420
 Qy 452 HPNSGLATIMSDBGKMKMYVGGKAKAGVWRDITGNRSYVTITNADGKGFVNGGAVS 511
 Db 421 HPNSGLATIMSDBGKMKMYVGGKAKAGVWRDITGNRSYVTITNADGKGFVNGGAVS 480
 Qy 512 VVWVQ 516
 Db 481 VVWVQ 485

RESULT 10
 US-09-925-576C-2
 ; Sequence 2, Application US/09925576C
 ; Publication No. US20030129718A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Andersen, Carsten
 ; APPLICANT: Borchert, Torben Vedel
 ; APPLICANT: Nielsen, Bjarne Ronfeldt
 ; TITLE OF INVENTION: Amylase Variants
 ; FILE REFERENCE: 10004.204-US
 ; CURRENT APPLICATION NUMBER: US/09/925,576C
 ; CURRENT FILING DATE: 2001-08-09
 ; NUMBER OF SEQ ID NOS: 20
 ; SOFTWARE: Patentin version 3.1
 ; SEQ ID NO 2
 ; LENGTH: 485
 ; TYPE: PRT
 ; ORGANISM: Bacillus sp.
 ; US-09-925-576C-2

Query Match 91.3%; Score 2613; DB 10; Length 485;

Best Local Similarity 95.1%; Pred. No. 9,7e-218;
Matches 461; Conservative 16; Mismatches 8; Indels 0; Gaps 0;

```
QY 32 HHNGTGMQYFEMHLPNDGNHNRRLRDDAANLKSKITAVWIPPAWKTSQNDVGYGA 91
DB 1 HHNGTGMQYFEMHLPNDGNHNRRLRDDAANLKSKITAVWIPPAWKTSQNDVGYGA 60
QY YDLYDGEFNQKGTVRTKXGTSQLOGAVTSLKNNGIQYGVVMMHKGADGTELVNAV 151
DB YDLYDGEFNQKGTVRTKXGTSQLOGAVTSLKNNGIQYGVVMMHKGADGTELVNAV 120
QY 152 EVNRSNRNOEISGEYTIEMWTKFDFPGRGNTSHNFKRWYHFDGTDMDQSRQONKIYKF 211
DB 121 EVNRSNRNOEISGEYTIEMWTKFDFPGRGNTSHNFKRWYHFDGTDMDQSRQONKIYKF 180
QY 212 RGTGKAMDEVDIENGNYDYLMADIDMDHPEVINELRWGWYTTNLMDGRIDAVKH 271
DB 181 RGTGKAMDEVDIENGNYDYLMADIDMDHPEVINELRWGWYTTNLMDGRIDAVKH 240
QY 272 IKYSYTRDMLTHVRNTTGKMPFAVAFWKNDLALIENTYLNKTSNMNSVDFVPLHYNLVNA 331
DB 241 IKYSYTRDMLTHVRNTTGKMPFAVAFWKNDLALIENTYLNKTSNMNSVDFVPLHYNLVNA 300
QY 332 SNSGGYFDMRNILNGSVQKHPIHAYTFVNDHDSQGEALSFVQSWFKPLAYALVLTRE 391
DB 301 SNSGGYFDMRNILNGSVQKHPIHAYTFVNDHDSQGEALSFVQSWFKPLAYALVLTRE 360
QY 392 QGYPSVFGDYGIPIPHGVPSMKSIDPLLOARQTYAYGTQHDYFPHDDIIGWTRGDS 451
DB 361 QGYPSVFGDYGIPIPHGVPSMKSIDPLLOARQTYAYGTQHDYFPHDDIIGWTRGDS 420
QY 452 HPNSGLATTMSDGGKMKMYVGKHKAGVWRDITGNBSGTVTINADGKNFTVNGGAVS 511
DB 421 HPNSGLATTMSDGGKMKMYVGKHKAGVWRDITGNBSGTVTINADGKNFTVNGGAVS 480
QY 512 VVWKQ 516
DB 481 VVWKQ 485
```

RESULT 11
US-10-025-648-1
Sequence 1, Application US/10025648
Publication No. US20030064908A1
GENERAL INFORMATION:

APPLICANT: Bisgard-Frantzen, Henrik
Svendsen, Allan
Borchert, Torden Vedel
TITLE OF INVENTION: AMYLASE VARIANTS
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Novo Nordisk of North America, Inc.
STREET: 405 Lexington Avenue, Suite 6400
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10174-6401

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/025,648
FILING DATE: 19-Dec-2001
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/600,656
FILING DATE: 13-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: Lambiris, Elias J.
REGISTRATION NUMBER: 33,728
REFERENCE/DOCKET NUMBER: 4318, 204-US

TELECOMMUNICATION INFORMATION:

TELEPHONE: 212 867 0123
TELEFAX: 212 867 0298

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:
LENGTH: 485 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-025-648-1

Query Match 91.3%; Score 2613; DB 14; Length 485;
Best Local Similarity 95.1%; Pred. No. 9,7e-218;
Matches 461; Conservative 16; Mismatches 8; Indels 0; Gaps 0;

```
QY 32 HHNGTGMQYFEMHLPNDGNHNRRLRDDAANLKSKITAVWIPPAWKTSQNDVGYGA 91
DB 1 HHNGTGMQYFEMHLPNDGNHNRRLRDDAANLKSKITAVWIPPAWKTSQNDVGYGA 60
QY 92 YDLYDGEFNQKGTVRTKXGTSQLOGAVTSLKNNGIQYGVVMMHKGADGTELVNAV 151
DB 61 YDLYDGEFNQKGTVRTKXGTSQLOGAVTSLKNNGIQYGVVMMHKGADGTELVNAV 120
QY 152 EVNRSNRNOEISGEYTIEMWTKFDFPGRGNTSHNFKRWYHFDGTDMDQSRQONKIYKF 211
DB 121 EVNRSNRNOEISGEYTIEMWTKFDFPGRGNTSHNFKRWYHFDGTDMDQSRQONKIYKF 180
QY 212 RGTGKAMDEVDIENGNYDYLMADIDMDHPEVINELRWGWYTTNLMDGRIDAVKH 271
DB 181 RGTGKAMDEVDIENGNYDYLMADIDMDHPEVINELRWGWYTTNLMDGRIDAVKH 240
QY 272 IKYSYTRDMLTHVRNTTGKMPFAVAFWKNDLALIENTYLNKTSNMNSVDFVPLHYNLVNA 331
DB 241 IKYSYTRDMLTHVRNTTGKMPFAVAFWKNDLALIENTYLNKTSNMNSVDFVPLHYNLVNA 300
QY 332 SNSGGYFDMRNILNGSVQKHPIHAYTFVNDHDSQGEALSFVQSWFKPLAYALVLTRE 391
DB 301 SNSGGYFDMRNILNGSVQKHPIHAYTFVNDHDSQGEALSFVQSWFKPLAYALVLTRE 360
QY 392 QGYPSVFGDYGIPIPHGVPSMKSIDPLLOARQTYAYGTQHDYFPHDDIIGWTRGDS 451
DB 361 QGYPSVFGDYGIPIPHGVPSMKSIDPLLOARQTYAYGTQHDYFPHDDIIGWTRGDS 420
QY 452 HPNSGLATTMSDGGKMKMYVGKHKAGVWRDITGNBSGTVTINADGKNFTVNGGAVS 511
DB 421 HPNSGLATTMSDGGKMKMYVGKHKAGVWRDITGNBSGTVTINADGKNFTVNGGAVS 480
QY 512 VVWKQ 516
DB 481 VVWKQ 485
```

RESULT 12
US-10-184-771-12
Sequence 12, Application US/10184771
Publication No. US20030170769A1
GENERAL INFORMATION:

APPLICANT: Svendsen, Allan
Borchert, Torden Vedel
TITLE OF INVENTION: Alpha-Amylase Mutants
FILE REFERENCE: 076/1f216-US2
CURRENT APPLICATION NUMBER: US/10/184,771
FILING DATE: 2002-06-28
PRIOR APPLICATION NUMBER: US/09/636,252

PRIOR FILING DATE: 2000-08-10

PRIOR APPLICATION NUMBER: 08/683,838

PRIOR FILING DATE: 1996-07-18
NUMBER OF SEQ ID NOS: 16
SOFTWARE: FaetsSeq for Windows Version 3.0
SEQ ID NO 12

LENGTH: 485
TYPE: PRT
ORGANISM: Bacillus
US-10-184-771-12

Query Match 91.3%; Score 2613; DB 14; Length 485;
Best Local Similarity 95.1%; Pred. No. 9.7e-218;
Matches 461; Conservative 16; Mismatches 8; Indels 0; Gaps 0;

```

QY 32 HHNGTNGTMQYFEWHLNDGNHNRRLRDDAANLKSKITAVWIPPAKGTSONDVGYGA 91
DB 1 HHNGTNGTMQYFEWHLNDGNHNRRLRDDAANLKSKITAVWIPPAKGTSONDVGYGA 60
QY 92 YDLVDLGEFNOKGTVRTKYGTRSOLOGAVTSLKNNGIQVGDVVMNHKGADGTEMVAV 151
DB 61 YDLVDLGEFNOKGTVRTKYGTRNOLOAAVTSLKNNGIQVGDVVMNHKGADGTEIVAV 120
QY 152 EVNSNRNOEISGEYTIEMWTKFDFPGKGNTHSNFKRWYHFDGTDMDOSROLQNKIKYF 211
DB 121 EVNSNRNOEISGEYTIEMWTKFDFPGKGNTHSNFKRWYHFDGTDMDOSROLQNKIKYF 180
QY 212 RGTGKAMDWEVDTENGVNDYLMYADVMDHBEVHELRNMGVWYNTLTLDGFRIDAVKH 240
DB 181 RGTGKAMDWEVDTENGVNDYLMYADVMDHBEVHELRNMGVWYNTLTLDGFRIDAVKH 240
QY 272 IKSYTRDMLTHVNTTGGKPMFAVAEFWKNDLAIENYLNKTSWNHSEVDVPLHYNLVNA 331
DB 241 IKSYTRDMLTHVNTTGGKPMFAVAEFWKNDLAIENYLNKTSWNHSEVDVPLHYNLVNA 300
QY 332 SNSGGEYDMRNILNGSVQKPHIAVTFVDNHDSPGEALESFYQSWFKPLAYALITRE 391
DB 301 SNSGGEYDMRNILNGSVQKPHIAVTFVDNHDSPGEALESFYQSWFKPLAYALITRE 360
QY 392 QGYSVFYGDYGGIPTHGVPBMSKIDPLQARQTYAVGTQHDYFDHDDIIGWTRBGSS 451
DB 361 QGYSVFYGDYGGIPTHGVPBMSKIDPLQARQTYAVGTQHDYFDHDDIIGWTRBGSS 420
QY 452 HPNSGLATINSDDGGKMMYVGGKAGQVWRDITGNRSGVTITNADGNGFTNGGAVS 511
DB 421 HPNSGLATINSDDGGKMMYVGGKAGQVWRDITGNRSGVTITNADGNGFTNGGAVS 480
QY 512 VVWQK 516
DB 481 VVWQK 485

```

RESULT 13
US-10-327-837-1
Sequence 1, Application US/10327837
Publication No. US20030211958A1

GENERAL INFORMATION:

APPLICANT: Svendsen, Allan
APPLICANT: Borchert, Torben Vedel
APPLICANT: Bisgaard-Frantzen Henrik
APPLICANT: Oustrup, Helle
APPLICANT: Nielsen, Bjarne Ronfeldt
APPLICANT: Nielsen, Vibeke Skovgaard
APPLICANT: Hoeck, Lisbeth Hedegeaard
TITLE OF INVENTION: Novel -Amylase And -Amylase Mutants
FILE REFERENCE: 5276.400-US
CURRENT APPLICATION NUMBER: US/10/327,837
PRIOR FILING DATE: 2002-12-23
PRIOR APPLICATION NUMBER: US/09/290,734
NUMBER OF SEQ ID NOS: 35
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 1
LENGTH: 485
TYPE: PRT
ORGANISM: Bacillus sp.
US-10-327-837-1

Query Match 91.3%; Score 2613; DB 15; Length 485;

Best Local Similarity 95.1%; Pred. No. 9.7e-218;
Matches 461; Conservative 16; Mismatches 8; Indels 0; Gaps 0;

```

QY 32 HHNGTNGTMQYFEWHLNDGNHNRRLRDDAANLKSKITAVWIPPAKGTSONDVGYGA 91
DB 1 HHNGTNGTMQYFEWHLNDGNHNRRLRDDAANLKSKITAVWIPPAKGTSONDVGYGA 60
QY 92 YDLVDLGEFNOKGTVRTKYGTRSOLOGAVTSLKNNGIQVGDVVMNHKGADGTEMVAV 151
DB 61 YDLVDLGEFNOKGTVRTKYGTRNOLOAAVTSLKNNGIQVGDVVMNHKGADGTEIVAV 120
QY 152 EVNSNRNOEISGEYTIEMWTKFDFPGKGNTHSNFKRWYHFDGTDMDOSROLQNKIKYF 211
DB 121 EVNSNRNOEISGEYTIEMWTKFDFPGKGNTHSNFKRWYHFDGTDMDOSROLQNKIKYF 180
QY 212 RGTGKAMDWEVDTENGVNDYLMYADVMDHBEVHELRNMGVWYNTLTLDGFRIDAVKH 240
DB 181 RGTGKAMDWEVDTENGVNDYLMYADVMDHBEVHELRNMGVWYNTLTLDGFRIDAVKH 240
QY 272 IKSYTRDMLTHVNTTGGKPMFAVAEFWKNDLAIENYLNKTSWNHSEVDVPLHYNLVNA 331
DB 241 IKSYTRDMLTHVNTTGGKPMFAVAEFWKNDLAIENYLNKTSWNHSEVDVPLHYNLVNA 300
QY 332 SNSGGEYDMRNILNGSVQKPHIAVTFVDNHDSPGEALESFYQSWFKPLAYALITRE 391
DB 301 SNSGGEYDMRNILNGSVQKPHIAVTFVDNHDSPGEALESFYQSWFKPLAYALITRE 360
QY 392 QGYSVFYGDYGGIPTHGVPBMSKIDPLQARQTYAVGTQHDYFDHDDIIGWTRBGSS 451
DB 361 QGYSVFYGDYGGIPTHGVPBMSKIDPLQARQTYAVGTQHDYFDHDDIIGWTRBGSS 420
QY 452 HPNSGLATINSDDGGKMMYVGGKAGQVWRDITGNRSGVTITNADGNGFTNGGAVS 511
DB 421 HPNSGLATINSDDGGKMMYVGGKAGQVWRDITGNRSGVTITNADGNGFTNGGAVS 480
QY 512 VVWQK 516
DB 481 VVWQK 485

```

RESULT 14
US-10-327-837-7
Sequence 7, Application US/10327837
Publication No. US20030211958A1

GENERAL INFORMATION:

APPLICANT: Svendsen, Allan
APPLICANT: Borchert, Torben Vedel
APPLICANT: Bisgaard-Frantzen Henrik
APPLICANT: Oustrup, Helle
APPLICANT: Nielsen, Bjarne Ronfeldt
APPLICANT: Nielsen, Vibeke Skovgaard
APPLICANT: Hoeck, Lisbeth Hedegeaard
TITLE OF INVENTION: Novel -Amylase And -Amylase Mutants
FILE REFERENCE: 5276.400-US
CURRENT APPLICATION NUMBER: US/10/327,837
PRIOR FILING DATE: 2002-12-23
PRIOR APPLICATION NUMBER: US/09/290,734
NUMBER OF SEQ ID NOS: 35
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 7
LENGTH: 485
TYPE: PRT
ORGANISM: Bacillus sp.
US-10-327-837-7

Query Match 91.3%; Score 2613; DB 15; Length 485;
Best Local Similarity 95.1%; Pred. No. 9.7e-218;
Matches 461; Conservative 16; Mismatches 8; Indels 0; Gaps 0;

```

QY 32 HHNGTNGTMQYFEWHLNDGNHNRRLRDDAANLKSKITAVWIPPAKGTSONDVGYGA 91
DB 1 HHNGTNGTMQYFEWHLNDGNHNRRLRDDAANLKSKITAVWIPPAKGTSONDVGYGA 60

```

```

QY 92 YDIYDLGEFNQKGTVRTKIGTSSQLQAVTSLKNGGIQYGVVYVNHKGGADGTENVAV 151
DB 61 YDIYDLGEFNQKGTVRTKIGTSSQLQAAVTSLKNGGIQYGVVYVNHKGGADGTENVAV 120
QY 152 EVNRSNRNOEISGEYTIEMATKEDPFGKGNTHSNFKRWYHFDGTMDOSROLQNKIYKF 211
DB 121 EVNRSNRNOEISGEYTIEMATKEDPFGKGNTHSNFKRWYHFDGTMDOSROLQNKIYKF 180
QY 212 RGTGKAMDWEVDIENGNDYILMYADIMDHPVINELRNMGVYNTNLTLDGFRIDAVKH 271
DB 181 RGTGKAMDWEVDIENGNDYILMYADIMDHPVINELRNMGVYNTNLTLDGFRIDAVKH 240
QY 272 IKYSYTRDMLTHVRNTTGKMPFAVAFWKNDLAIENYLNKTSNHSVDPVPLHYNLYNA 331
DB 241 IKYSYTRDMLTHVRNTTGKMPFAVAFWKNDLAIENYLNKTSNHSVDPVPLHYNLYNA 300
QY 332 SNSGGYFDMRNILNGSVVQKHPHIAVTFVNDHDSQGEALLESFVQSWFKPLAYALITRE 391
DB 301 SNSGGYFDMRNILNGSVVQKHPHIAVTFVNDHDSQGEALLESFVQSWFKPLAYALITRE 360
QY 392 OGYPVYFGDYGIPTHGVPMSKSIDPLQARQYAYGTQHDYFDHDIIGWTRGDS 451
DB 361 OGYPVYFGDYGIPTHGVPMSKSIDPLQARQYAYGTQHDYFDHDIIGWTRGDS 420
QY 452 HPSGLATIMSDPGGNKMYVGNKAGQVWRDITGNRSGVTITNDGNGFTVNGAYS 511
DB 421 HPSGLATIMSDPGGNKMYVGNKAGQVWRDITGNRSGVTITNDGNGFTVNGAYS 480
QY 512 VWYKQ 516
DB 481 VWYKQ 485

```

RESULT 15
US-10-665-667-1
; Sequence 1, Application US/10665667
; Publication No. US20040038368A1
; GENERAL INFORMATION:
; APPLICANT: Borchert, Torben V.
; APPLICANT: Svendsen, Allan
; APPLICANT: Andersen, Carsten
; APPLICANT: Nielsen, Bjarne
; APPLICANT: Miesse, Torben L.
; APPLICANT: Kjaerulf, Soren
; TITLE OF INVENTION: Alpha-Amulase Mutants
; FILE REFERENCE: 5368.200-US
; CURRENT APPLICATION NUMBER: US/10/665,667
; PRIOR FILING DATE: 2003-09-19
; PRIOR APPLICATION NUMBER: US/09/769,864
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 09/183,412
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 485
; TYPE: PRT
; ORGANISM: Bacillus
US-10-665-667-1

Query Match 91.3%; Score 2613; DB 15; Length 485;
Best Local Similarity 95.1%; Pred. No. 9.7e-218;
Matches 461; Conservative 16; Mismatches 8; Indels 0; Gaps 0;

```

QY 32 HHNGTNGTMMQYFEWHLNDGNHNRRLRDDAANLKSIGITAVWLPAMKGTSONDVGYGA 91
DB 1 HHNGTNGTMMQYFEWHLNDGNHNRRLRDDAANLKSIGITAVWLPAMKGTSONDVGYGA 60
QY 92 YDIYDLGEFNQKGTVRTKIGTSSQLQAVTSLKNGGIQYGVVYVNHKGGADGTENVAV 151
DB 61 YDIYDLGEFNQKGTVRTKIGTSSQLQAAVTSLKNGGIQYGVVYVNHKGGADGTENVAV 120

```

```

QY 152 EVNRSNRNOEISGEYTIEMATKEDPFGKGNTHSNFKRWYHFDGTMDOSROLQNKIYKF 211
DB 121 EVNRSNRNOEISGEYTIEMATKEDPFGKGNTHSNFKRWYHFDGTMDOSROLQNKIYKF 180
QY 212 RGTGKAMDWEVDIENGNDYILMYADIMDHPVINELRNMGVYNTNLTLDGFRIDAVKH 271
DB 181 RGTGKAMDWEVDIENGNDYILMYADIMDHPVINELRNMGVYNTNLTLDGFRIDAVKH 240
QY 272 IKYSYTRDMLTHVRNTTGKMPFAVAFWKNDLAIENYLNKTSNHSVDPVPLHYNLYNA 331
DB 241 IKYSYTRDMLTHVRNTTGKMPFAVAFWKNDLAIENYLNKTSNHSVDPVPLHYNLYNA 300
QY 332 SNSGGYFDMRNILNGSVVQKHPHIAVTFVNDHDSQGEALLESFVQSWFKPLAYALITRE 391
DB 301 SNSGGYFDMRNILNGSVVQKHPHIAVTFVNDHDSQGEALLESFVQSWFKPLAYALITRE 360
QY 392 OGYPVYFGDYGIPTHGVPMSKSIDPLQARQYAYGTQHDYFDHDIIGWTRGDS 451
DB 361 OGYPVYFGDYGIPTHGVPMSKSIDPLQARQYAYGTQHDYFDHDIIGWTRGDS 420
QY 452 HPSGLATIMSDPGGNKMYVGNKAGQVWRDITGNRSGVTITNDGNGFTVNGAYS 511
DB 421 HPSGLATIMSDPGGNKMYVGNKAGQVWRDITGNRSGVTITNDGNGFTVNGAYS 480
QY 512 VWYKQ 516
DB 481 VWYKQ 485

```

Search completed: May 2, 2005, 22:02:08
Job time : 63 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 2, 2005, 21:33:38 ; Search time 23 Seconds

(without alignment)
2158.602 Million cell updates/sec

Title: US-08-952-741-2

Sequence: 1 MKLHNRIISVLTLLLAVALV.....ADGKGNFTVNGAVSWVKQ 516

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : PIR 79:*

1: p1r1:*

2: p1r2:*

3: p1r3:*

4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2438.5	85.2	518	1 A27705	alpha-amyase (EC
2	1942	67.9	512	1 ALBSL	alpha-amyase (EC
3	1924.5	67.2	549	1 A24541	alpha-amyase (EC
4	1909.5	66.7	549	1 A24549	alpha-amyase (EC
5	1908.5	66.7	549	1 A24436	alpha-amyase (EC
6	1845.5	64.5	514	1 ALBSN	alpha-amyase (EC
7	1837	64.2	548	1 ALBSF	alpha-amyase (EC
8	1347	47.1	493	2 G51713	alpha-amyase (EC
9	1240	43.3	484	2 G95160	alpha-amyase (EC
10	1240	43.3	492	2 AH2079	alpha-amyase (EC
11	1238	43.3	484	2 C68781	alpha-amyase (EC
12	1133	39.6	491	2 C68781	alpha-amyase (EC
13	1090.5	38.1	506	2 G98247	alpha-amyase (EC
14	1084	37.9	495	2 AD3038	alpha-amyase (EC
15	1053	36.8	494	1 B45738	alpha-amyase (EC
16	1045	36.5	494	2 AD0751	alpha-amyase (EC
17	1025	35.8	495	2 B90962	alpha-amyase (EC
18	1022	35.7	495	1 A45738	alpha-amyase (EC
19	1006	35.2	495	2 B85810	alpha-amyase (EC
20	393.5	13.7	217	2 A19506	beta-amyase (EC 3
21	323	11.3	1196	2 A29130	alpha-amyase (EC
22	312.5	10.9	482	2 S31478	glucan 1,4-alpha-m
23	304	10.6	551	2 S05667	alpha-amyase (EC
24	297.5	10.4	440	2 S14958	alpha-amyase (EC
25	295	10.3	421	2 S10514	alpha-amyase (EC
26	287.5	10.0	428	2 T05521	alpha-amyase (EC
27	287	10.0	423	2 T09942	alpha-amyase (EC
28	286.5	10.0	826	2 B96720	probable alpha-amy
29	285	10.0	547	2 A32803	glucan 1,4-alpha-m

30	284.5	9.9	713	2 S09196	cyclomaltodextrin
31	279.5	9.8	438	2 S14957	alpha-amyase (EC
32	278	9.7	713	1 ALBSG7	cyclomaltodextrin
33	277	9.7	713	1 ALBSG1	cyclomaltodextrin
34	277	9.7	718	1 ALBSG3	cyclomaltodextrin
35	275	9.6	712	1 ALBSG3	cyclomaltodextrin
36	274.5	9.6	713	2 A58800	cyclomaltodextrin
37	272	9.5	718	1 ALBSG6	cyclomaltodextrin
38	270	9.4	528	1 ALBSK	alpha-amyase (EC
39	269.5	9.4	437	2 S14956	alpha-amyase (EC
40	268.5	9.4	435	2 UC7137	alpha-amyase (EC
41	268.5	9.4	435	2 S12625	alpha-amyase (EC
42	268.5	9.4	438	1 ALBH	alpha-amyase (EC
43	267.5	9.3	710	2 S63598	cyclomaltodextrin
44	264	9.2	504	2 A55861	alpha-amyase (EC
45	263.5	9.2	428	2 S10013	alpha-amyase (EC

ALIGNMENTS

RESULT 1

A27705 alpha-amyase (EC 3.2.1.1) precursor - Bacillus sp.

N:Alternate names: 1,4-alpha-D-glucan glucanohydrolase; G6-amyase

C:Species: Bacillus sp.

C:Date: 31-Mar-1989 #sequence_revision 18-Aug-1995 #text_change 16-Aug-2004

C:Accession: A27705

R:Rtsukamoto, A.; Kimura, K.; Ishii, Y.; Takano, T.; Yamane, K.

Biochem. Biophys. Res. Commun. 151, 25-31, 1988

A:Title: Nucleotide sequence of the maltohexose-producing amyase gene from an alkaloph

A:Reference number: A27705; MUID:88162814; PMID:3258152

A:Accession: A27705

A:Molecule type: DNA

A:Residues: 1-518 <TSU>

A:Cross-references: UNIPROT:P19571; GB:M1862; NID:G142496; PIDN:AAA22231.1; PID:G142497

A:Experimental source: chromosomal DNA of strain 707

A>Note: amino end of mature protein also determined

C:Comment: This is the smallest of five starch-hydrolyzing enzymes from this organism.

C:Function:

A:Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds

A:Pathway: glycogen/starch degradation

C:Superfamily: Alpha-amyase, amyloliquefaciens type; alpha-amyase, core homology

C:Keywords: extracellular protein; glycosidase; hydrolase; polysaccharide degradation

F:1-33/Domain: signal sequence #status predicted <Sig>

F:34-518/Product: alpha-amyase #status experimental <Mat>

F:236-359/Domain: alpha-amyase core homology <AMY>

F:139,238,273/Binding site: calcium (Asn, Asp, His) #status predicted

F:269,299,366/Active site: Asp, Glu, Asp #status predicted

Query Match 85.2%; Score 2438.5; DB 1; Length 518;

Best Local Similarity 83.7%; Pred. No. 3.7e-158;

Matches 426; Conservative 42; Mismatches 40; Indels 1; Gaps 1;

QY	8	ISVLTLLLAVALVFPYMTPEAOAHNGTGMQYEMHLPNDGNHNRRLRDAANIKS	67
DB	11	LSILAFLLVLTTS-PTFLVDVEAHNGTGMQYEMHLPNDGNHNRRLNSDANIKS	69
QY	68	KGITAVWIPPAWKSTQNDVGYGAYDYLDEFNQKGTVRKTKYGRSOLQGAVTSLKNG	127
DB	70	KGITAVWIPPAWKASQNDVGYGAYDYLDEFNQKGTVRKTKYGRSOLQAAVTSLKNG	129
QY	128	IQVYGVVNMHKGADGTEVNAVEVRSNRNOISGEYITTEAMTKDFPGRGTHSNFK	187
DB	130	IQVYGVVNMHKGADGTEVNAVEVRSNRNOISGEYITTEAMTRDFPGRGTHSNFK	189
QY	188	WRWHPFGTMDOSROCNKTYKRGKAMDWEVDLENGYDYLMAADIDMDHPEVINE	247
DB	190	WRWHPFGVDDQSRRLNRRKTYKRGKAMDWEVDLENGYDYLMAADIDMDHPEVINE	249
QY	248	LRNNGVWYTNLTNDGRIDAVKIKYSYTRDWLTTHVYRNTTGKMPFAVEFWKNDLAIIE	307
DB	250	LRNNGVWYTNLTNDGRIDAVKIKYSYTRDWLTTHVYRNTTGKMPFAVEFWKNDLAIIE	309

Qy	306	NYLNTKSNMHSVDVDELPHNLVNSNSGGYFEMERINILNGSVQKHPIHAFVFNHNSOP	367
	310	NYLQKTNMNSVDVDELPHNLVNSKSGGNYMERNIENGIVQRRHPSHAFVFNHNSOP	369
Db	368	GEALSFVSOWSFKPLAVALILTRQOGYPSVFQGDYVGIPTGVPSPMSKIDPLLOAQOTY	427
Qy	370	EEALHSEVSEWMEFKPLAVALILTRQOGYPSVFQGDYVGIPTGVPAMRKRKIDPILAEQKY	429
Db	428	AYGTQHDYFEDHDIICWTRBGSSHPNSGLATIMSDGQGNKMYGVGKHKAQYWRDITG	487
Qy	430	AYKQNDYLDLHHNIIEMTREGMTAFHPNSGLATIMSDGAGSSXMFVGNKKAQYWSIDTG	489
Db	488	NBSGVTINADGWNFTVNGAVSVWYVKQ	516
Qy	490	NRTGVTINADGWNFSVNGSVASVWYVK	518

RESULT 2

alpha-amylase (EC 3.2.1.1) precursor [validated] - *Bacillus licheniformis*
M:Alternate names: 1,4-alpha-D-glucan glucanohydrolase
C:Species: *Bacillus licheniformis*
C:Date: 30-Jun-1997 #sequence revision 24-Apr-1998 #text change 16-Aug-2004
A:Accession: A91997; B24497, A91796; A21663; I39772; A26151; S53788; A00844
R:Yukit, T.; Nomura, T.; Teuka, H.; Tsuboi, A.; Yamagata, H.; Tsukagochi, N.; Uda, S.
J. Biochem. 98, 1147-1156, 1985
A:Title: Complete nucleotide sequence of a gene coding for heat- and pH-stable alpha-amylase deduced from the DNA sequences.
A:Reference number: A91997; MUID:86111694; PMID:2418011
A:Accession: A91997
A:Molecule type: DNA
A:Residues: 1-162; 'R', 164-512 <YNU>
A:Cross-references: UNIPROT:P06278; UNIPROT:Q45283; GB:X03236; NID:G39551; PIDN:CAA26981
A:Experimental source: ATCC 27811
R:Gay, G.L.; Mainzer, S.E.; Rey, M.W.; Lamsa, M.H.; Kindle, K.L.; Carmona, C.; Reguad, J. Bacteriol. 166, 635-643, 1986
A:Title: Structural genes encoding the thermophilic alpha-amylases of *Bacillus stearothermophilus*
A:Reference number: A91817; MUID:86195857; PMID:3009417
A:Accession: B24549
A:Molecule type: DNA
A:Residues: 1-338; 'G', 340-348, 'S', 350-512 <GRA>
A:Cross-references: GB:M13256; NID:g142510; PIDN:AAA22240.1; PID:g142511
A:Experimental source: NCIB 8061
R:Stephens, M.A.; Orlepp, S.A.; Ollington, J.F.; McConnell, D.J.
J. Bacteriol. 159, 369-372, 1984
A:Title: Nucleotide sequence of the 5' region of the *Bacillus licheniformis* alpha-amylase
A:Reference number: A91796; MUID:84185455; PMID:6609154
A:Accession: A91796
A:Molecule type: DNA
A:Residues: 1-104 <STE>
A:Cross-references: GB:K01984; NID:g142432; PIDN:AAA22193.1; PID:g142433
R:Slbakov, M.; Paiva, I.
Eur. J. Biochem. 145, 567-572, 1984
A:Title: Isolation and the 5'-end nucleotide sequence of *Bacillus licheniformis* alpha-amylase
A:Reference number: A21663; MUID:85076654; PMID:6334606
A:Accession: A21663
A:Molecule type: DNA
A:Residues: 1-3; 'H', 5-12, 'P', 14-47, 'R', 49-61, 'V', 63, 'D', 65-67, 'VA', 70-71, 'S', 73-80, 'D', 81-82
A:Experimental source: Chromosomal DNA of ATCC 14580
A:Note: the authors translated the codon CGT for residue 48 as Gly and GAC for residue 60
R:Loide, B.M.; Chambliss, G.H.; McConnell, D.J.
J. Bacteriol. 171, 2435-2442, 1989
A:Title: *Bacillus licheniformis* alpha-amylase gene, *amyL*, is subject to promoter-independent regulation
A:Reference number: I39773; MUID:89213924; PMID:2540150
A:Accession: I39774
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-29 <LAO>
A:Cross-references: GB:M26412; NID:G341477; PIDN:AAA22237.1; PID:G516590
R:Jorgensen, P.L.; Hansen, C.K.; Poulsen, G.B.; Diderichsen, B.
Gene 96, 37-41, 1990
A:Title: In vivo genetic engineering: homologous recombination as a tool for plasmid con-

QY	361	DNHSQPGEALESFVQSNKPELAVALILTRBOGYSEVFQDYYGIPRHG----	VSQMS	415
DB	294	NDLGLALEVNLKTNFNHSEVDFVPLHYQFHAASIQGGGYDWRKLLNSVVSKEHPLKAVTFV		353
QY	301	NDLAAIEVNLKTNMNSHSEVDFVPLHYNLNASNSGGYFDMKRLNLSVVOKPIHATFV		360
DB	234	HPDVAAIEIKMGTWYANELQDGFRLDAVKHKEFSLRDMVHVKRETKGEMFTVAELWQ		293
QY	241	HPEVINELNKQWVWYTNLTNLQGFRLDAVKHKEFSLRDMVHVKRETKGEMFTVAELWQ		300
DB	177	STYSPFKMHWYFDDGDMQESRKL-NRIKFO--GAMQWESNENGNDYLYMADIDYD		233
QY	181	NTHSNFKRWYHFFDGDWQSOLOKIKYKFRGTGAMMEVDLENGNYLYMADIDMD		240
DB	117	KSLHSRDLNVGDVYINHKGADATEDVTAVEYDPAIDRRKVIQSEHLIKAMTFHFPGRG		176
QY	121	TSLKNGIQVYGVVMMHKGADGTEMVNAVEVNSRNNQEISGEYITEAWYKFPDPGRG		180
DB	57	DSAYLAHNGITAVMIPPAKGTSGQADVGAYDYLVDGERHQGQYRTKTKGTGELQSAI		116
QY	61	DAANFKSKGITAVMIPPAKGTSGQADVGAYDYLVDGERHQGQYRTKTKGTGELQSAI		120
DB	1	MKQQRLLVRLTLTLFALFLPLPHSAAAAA---NINGTLMQFEMWEPDQGHKSLQN		56
QY	1	MCLEHRIISVLTLLLAVALVFPYMTPEPAQAHNNGTGMQYFEMHLPDNGHNMNLRD		60
DB	347	Conservative	71; Mismatches	89; Indels
QY	67.9%;	Score 1942;	DB 1;	Length 512;
QY	Best Local Similarity	66.6%;	Pred. No. 2e-124;	
QY	Matches	347;	Conservative	71; Mismatches 89; Indels 14; Gaps 5;
QY	1	MCLEHRIISVLTLLLAVALVFPYMTPEPAQAHNNGTGMQYFEMHLPDNGHNMNLRD		60
QY	61	DAANFKSKGITAVMIPPAKGTSGQADVGAYDYLVDGERHQGQYRTKTKGTGELQSAI		120
QY	57	DSAYLAHNGITAVMIPPAKGTSGQADVGAYDYLVDGERHQGQYRTKTKGTGELQSAI		116
QY	121	TSLKNGIQVYGVVMMHKGADGTEMVNAVEVNSRNNQEISGEYITEAWYKFPDPGRG		180
QY	117	KSLHSRDLNVGDVYINHKGADATEDVTAVEYDPAIDRRKVIQSEHLIKAMTFHFPGRG		176
QY	181	NTHSNFKRWYHFFDGDWQSOLOKIKYKFRGTGAMMEVDLENGNYLYMADIDMD		240
QY	177	STYSPFKMHWYFDDGDMQESRKL-NRIKFO--GAMQWESNENGNDYLYMADIDYD		233
QY	241	HPEVINELNKQWVWYTNLTNLQGFRLDAVKHKEFSLRDMVHVKRETKGEMFTVAELWQ		300
QY	234	HPDVAAIEIKMGTWYANELQDGFRLDAVKHKEFSLRDMVHVKRETKGEMFTVAELWQ		293
QY	301	NDLAAIEVNLKTNMNSHSEVDFVPLHYNLNASNSGGYFDMKRLNLSVVOKPIHATFV		360
QY	294	NDLGLALEVNLKTNFNHSEVDFVPLHYQFHAASIQGGGYDWRKLLNSVVSKEHPLKAVTFV		353
QY	361	DNHSQPGEALESFVQSNKPELAVALILTRBOGYSEVFQDYYGIPRHG----	VSQMS	415

Db 354 DNHDTQPGSLESTVQVTEFKPLAVALFILTRESGYPOVFGYDMG--TKGDSOREIPALKH 411
 Qy 416 KIDPLIARQYAYGQHDYFDHDIIGWTRBGSSHPNSGLATIMSDPGKNKMYVQK 475
 Db 412 KIEPLIKAKQYAYGQHDYFDHDIIGWTRBGSSHPNSGLATITDGPAGAKMYVQK 471
 Qy 476 HKAQVWRDITGNRSQVITINADGNGFTVNGAVSVWV 516
 Db 472 QNAGETMHDITGNRSEPVINSEGMGEFVNGSVISIVQR 512

RESULT 3

A54541
 alpha-amylase (EC 3.2.1.1) precursor - Bacillus stearothermophilus (strain DN1792)
 N:Alternate names: 1,4-alpha-D-glucan glucanohydrolase
 C:Species: Bacillus stearothermophilus
 C:Date: 28-Oct-1994 #sequence_revision 18-Aug-1995 #text_change 16-Aug-2004
 C:Accession: A54541
 R:Jorgensen, P. L.; Poulsen, G. B.; Diderichsen, B.
 FEMS Microbiol. Lett. 77, 271-276, 1991
 A:Title: Cloning of a chromosomal alpha-amylase gene from Bacillus stearothermophilus.
 A:Reference number: A54541
 A:Accession: A54541
 A:Molecule type: DNA
 A:Residues: 1-549 <J0R>
 A:Cross-references: UNIPROT:Q9KMY6; UNIPROT:031193; GB:X59476
 A:Experimental source: chromosomal DNA of strain DN1792
 C:Comment: Alpha-amylase genes have been found on plasmids and in multiple copies on the C:Genetics:
 A:Start codon: GTG
 C:Function:
 A:Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
 A:Pathway: glycogen/starch degradation
 C:Superfamily: Alpha-amylase, amyloliquefaciens type; alpha-amylase core homology
 C:Keywords: extracellular protein; glycosidase; heat-stable protein; hydrolase; polysac
 F:1-34/Domains: signal sequence #status predicted <SIG>
 F:35-549/Product: alpha-amylase #status predicted <MNT>
 F:235-368/Domains: alpha-amylase core homology <AMY>
 F:113,237,272/Binding site: calcium (Asp, Asp, His) #status predicted
 F:266,298,365/Active site: Asp, Glu, Asp #status predicted

Query Match 67.2%; Score 1924.5; DB 1; Length 549;
 Best Local Similarity 66.0%; Pred. No. 3.4e-123;
 Matches 342; Conservative 74; Mismatches 95; Indels 7; Gaps 4;
 Qy 1 MCLNRII-----SVLLTLLAVALFPYMTBPAQAHNGTGMQYEMHLNDGNHNR 56
 Db 1 MLTFRIRIRKGMWFLAFLTLVSLFPC-TGQPAKA-AAPFNGTMMQYFEMVLPDGTLMT 58
 Qy 57 RLRDDAAMLSKGTAVWIIPAMKGTSONDVGAYDYLDGEFNOKGTVRKYGTSQQL 116
 Db 59 KVANEANLSSIGITALLPAPYKGTSSDVGYDYLDGEFNOKGTVRKYGTSQKQY 118
 Qy 117 QGAVTSLKNGIGIYGVGVVNMHKGADGTEWNAVEVRSNRNOISGEYITTEATKDF 176
 Db 119 LQATQAAAGQYADVVPFHKGADGTEWDAVEVNSDRNOISGTYOIQATKDF 178
 Qy 177 PGRGNTSNFKRWYHFDGTMDOSROLONKIYKRGTKGKAMWVDIENGNYDYLMYAD 236
 Db 179 PGRGNTYSSFKRWYHFDGVWDESRKL-SRIYKFRIGIKAMWDEVTENGNYDYLMYAD 237
 Qy 237 IDMHPEVINELRMGVYVYTNLMDGRIDAVHGIKSYTRDMLTHNRANTGKMPAVA 296
 Db 238 LDMHPEVYVTELKMGKRYVNTINDGRLAVHGIKSYTRDMLTHNRANTGKMPAVA 297
 Qy 297 EFMKNDLAIENYLNKTSWNHSEVDPVLAHNLVNASNGGYEDMKNILNGSVQKPTHA 356
 Db 298 EYMSWDIKLKNYITKTGTMSTLPDAPLHNFYTKSGGAFDKRTLTMTILMDQPLA 357
 Qy 357 VTFVNDHDSQGEALIESFVQSMFKPLAVALILTRBQGYPSVFGDYGIPTHGVSMSK 416
 Db 358 VTFVNDHDEPGALQSWVDWPFKPLAVALILTRBQGYPSVFGDYGIPTHGVSMSK 417

Qy 417 IDPLIARQYAYGQHDYFDHDIIGWTRBGSSHPNSGLATIMSDPGKNKMYVQK 476
 Db 418 IDPLIARQYAYGQHDYFDHDIIGWTRBGSTKPSGSLAALITDGPAGAKMYVQK 477
 Qy 477 KAGQVWRDITGNRSQVITINADGNGFTVNGAVSVWV 514
 Db 478 HKAQVYFDLTGNRSDVTITNSDGMGEFVNGSVSVWV 515

RESULT 4

A24549
 alpha-amylase (EC 3.2.1.1) precursor - Bacillus stearothermophilus (strain NZ-3)
 N:Alternate names: 1,4-alpha-D-glucan glucanohydrolase
 C:Species: Bacillus stearothermophilus
 C:Date: 30-Jun-1988 #sequence_revision 18-Aug-1995 #text_change 16-Aug-2004
 C:Accession: A24549; 139501; 139770
 C:Gray, G. L.; Mainzer, S. E.; Rey, M. W.; Lamsa, M. H.; Kindle, K. L.; Carmona, C.; Reguadt,
 J. Bacteriol. 166, 635-643, 1986
 A:Title: Structural genes encoding the thermophilic alpha-amylases of Bacillus stearothe
 A:Reference number: A24549
 A:Accession: A24549
 A:Molecule type: DNA
 A:Residues: 1-549 <GRA>
 A:Cross-references: GB:M3255; NID:G142512; PIDN:AAA22241.1; PID:G142513
 A:Experimental source: genomic DNA of strain NZ-3
 R:Satch, H.; Nishida, H.; Isono, K.
 U. Bacteriol. 170, 1034-1040, 1988
 A:Title: Evidence for movement of the alpha-amylase gene into two phylogenetically dista
 A:Reference number: 139501; MUID:88139156; PMID:3257753
 A:Accession: 139501
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 536-549 <RES>
 A:Cross-references: GB:M29577; NID:G142476; PIDN:AAA22225.1; PID:G142478
 A:Experimental source: strain DY-5
 A:Accession: 139770
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 536-549 <RE2>
 A:Cross-references: GB:M29578; NID:G142484; PIDN:AAA22228.1; PID:G142486
 A:Experimental source: strain 799
 A:Comment: Alpha-amylase genes have been found on plasmids and in multiple copies on the C:Genetics:
 A:Start codon: GTG
 C:Function:
 A:Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
 A:Pathway: glycogen/starch degradation
 C:Superfamily: Alpha-amylase, amyloliquefaciens type; alpha-amylase core homology
 C:Keywords: extracellular protein; glycosidase; heat-stable protein; hydrolase; polysac
 F:1-34/Domains: signal sequence #status predicted <SIG>
 F:35-549/Product: alpha-amylase #status predicted <MNT>
 F:235-368/Domains: alpha-amylase core homology <AMY>
 F:113,237,272/Binding site: calcium (Asp, Asp, His) #status predicted
 F:266,298,365/Active site: Asp, Glu, Asp #status predicted

Query Match 66.7%; Score 1909.5; DB 1; Length 549;
 Best Local Similarity 66.0%; Pred. No. 3.5e-122;
 Matches 341; Conservative 73; Mismatches 98; Indels 5; Gaps 3;
 Qy 1 MCLNRIISVLLTLLA---VAVLPYMTBPAQAHNGTGMQYEMHLNDGNHNR 57
 Db 1 MLTFRIRIRKGMWFLAFLTLVSLFPC-TGQPAKA-AAPFNGTMMQYFEMVLPDGTLMT 59
 Qy 58 LRDDAAMLSKGTAVWIIPAMKGTSONDVGAYDYLDGEFNOKGTVRKYGTSQQL 117
 Db 60 VANANLSSIGITALLPAPYKGTSSDVGYDYLDGEFNOKGTVRKYGTSQQL 119
 Qy 118 GAVTSLKNGIGIYGVGVVNMHKGADGTEWNAVEVRSNRNOISGEYITTEATKDFP 177
 Db 120 QATQAAAGQYADVVPFHKGADGTEWDAVEVNSDRNOISGTYOIQATKDFN 179
 Qy 178 GRGNTSNFKRWYHFDGTMDOSROLONKIYKRGTKGKAMWVDIENGNYDYLMYAD 237

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Db      180 GRGNTYSSEFKMRYHFDGVMDWSRKL-SRIYKFRIGKAMWEDVTENGNDYLMYADL 238
Qy      238 DMDHPEVINELRNWGWYNTNTLMDGFRIDAVYKHIXSYTRDWLTHVRNTTGPMFAVAE 297
Db      239 DMDHPEVINELRNWGWYNTNTLMDGFRIDAVYKHIXSYTRDWLTHVRNTTGPMFAVAE 298
Qy      298 FPKNDLALAIENYLNKTSNMHNSVDFDPLHYNLNANSGGYEDMRNLNLSVQKPHLHAV 357
Db      299 YMSYDINKLHNYITKTNGTMSLFDAPLHNFYASKSGGFDMSITLNNNTLMKDOPTLAV 358
Qy      358 TFPVNDHDSOGFALBSFVQSWFKPLAYALILTRGQYPSVFGDYGYGIPTHGVPMSKSKI 417
Db      359 TFPVNDHDSOGFALBSFVQSWFKPLAYALILTRGQYPSVFGDYGYGIPTHGVPMSKSKI 418
Qy      418 DPLQARQTYAYGTQHDYFDHHDIIIGWTRGSDSSHNSGSLATIMSDPGGNKMYVGRKH 477
Db      419 DPLQARQTYAYGTQHDYFDHHDIIIGWTRGSDSSHNSGSLATIMSDPGGNKMYVGRKH 478
Qy      478 AGQWRDITGNRSQVITINADGWNFTNGCAVSVMV 514
Db      479 AGQWRDITGNRSQVITINADGWNFTNGCAVSVMV 515

```

RESULT 5

```

A24436
alpha-amyase (EC 3.2.1.1) precursor - Bacillus stearothermophilus plasmid pAT5
N/Alternate names: 1,4-alpha-D-glucan glucanohydrolase
C/Species: Bacillus stearothermophilus
C/Date: 05-Jun-1987 #sequence_revision 18-Aug-1995 #text_change 16-Aug-2004
C/Accession: A24436; I39777
R/Nakajima, R.; Imanaka, T.; Alba, S.
J. Bacteriol. 163, 401-406, 1985
A/Reference number: A24436; MUID:85234394; PMID:3924897
A/Accession: A24436
A/Molecule type: DNA
A/Residues: 1-549 <NAX>
A/Cross-references: UNIPROT:P06279; GB:M11450
A/Experimental source: plasmid pAT5
A/Note: amino end of the mature protein also determined
R/Orgensen, P.L.; Hansen, C.K.; Poulsen, G.B.; Diderichsen, B.
Gene 96, 37-41, 1990
A/Title: In vivo genetic engineering: homologous recombination as a tool for plasmid con
A/Reference number: I39772; MUID:91092499; PMID:2265757
A/Accession: I39777
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-45 <RBS>
A/Cross-references: GB:M62638; NID:g142514; PIDN:AAA22242.1; PID:g142515
C/Comment: Alpha-amyase genes have been found on plasmids and in multiple copies on the
C/Genetics:
A/Genome: amyS
A/Genome: plasmid
A/Start codon: GTG
C/Function:
A/Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A/Pathway: glycogen/starch degradation
C/Superfamily: alpha-amyase, amyloliquefaciens type; alpha-amyase core homology
C/Keywords: extracellular protein; glycosylase; heat-stable protein; hydrolase; polysac
F/1-34/Domain: signal sequence #status predicted <SIG>
F/35-549/Product: alpha-amyase #status experimental <MAN>
F/335-368/Domain: alpha-amyase core homology <AMY>
F/339-237/Binding site: calcium (Asp, Asp, His) #status predicted
F/268,298,365/Active site: Asp, Glu, Asp #status predicted

```

```

Query Match      66.7%; Score 1908.5; DB 1; Length 549;
Best Local Similarity 65.6%; Pred. No. 4,1e-122;
Matches 339; Conservative 75; Mismatches 98; Indels 5; Gaps 3;

```

```

Qy      1 MKNHNTIS---VLLTLLAVAVLFPYMEBAQAHNGNTGTMQYFEMHLPDGNHNR 57
Db      1 MTFHRIIRKGMWFLAFLTLTLLFCPTGQPAKA-AAFPGTMMQYFEMWLPDDGTLTWK 59
Qy      58 LRDAANLMSKGTAAWIPAMKGTSONDVGYAYDLVDGFEFGKGTAVTKYGTSTQIQ 117

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Db      60 VANEANNLSSLGITLMLPFAKYSRSRDVSGVYDLYDLGFEFGKGAARTYGTAKQYL 119
Qy      118 GAVTSIKNNIGYGVYDVVNMHKGADGTEMVANAVERNNSNRQESGETTEAMTKFDP 177
Db      120 QAIQAAHAAQGVYADVVDVHDHKGADGTEMVANAVERNNSNRQESGETTEAMTKFDP 179
Qy      178 GRGNTHSNFKMRYHFDGVMDWSRKL-SRIYKFRIGKAMWEDVTENGNDYLMYADL 237
Db      180 GRGNTYSSEFKMRYHFDGVMDWSRKL-SRIYKFRIGKAMWEDVTENGNDYLMYADL 238
Qy      238 DMDHPEVINELRNWGWYNTNTLMDGFRIDAVYKHIXSYTRDWLTHVRNTTGPMFAVAE 297
Db      239 DMDHPEVINELRNWGWYNTNTLMDGFRIDAVYKHIXSYTRDWLTHVRNTTGPMFAVAE 298
Qy      298 FPKNDLALAIENYLNKTSNMHNSVDFDPLHYNLNANSGGYEDMRNLNLSVQKPHLHAV 357
Db      299 YMSYDINKLHNYITKTNGTMSLFDAPLHNFYASKSGGFDMSITLNNNTLMKDOPTLAV 358
Qy      358 TFPVNDHDSOGFALBSFVQSWFKPLAYALILTRGQYPSVFGDYGYGIPTHGVPMSKSKI 417
Db      359 TFPVNDHDSOGFALBSFVQSWFKPLAYALILTRGQYPSVFGDYGYGIPTHGVPMSKSKI 418
Qy      418 DPLQARQTYAYGTQHDYFDHHDIIIGWTRGSDSSHNSGSLATIMSDPGGNKMYVGRKH 477
Db      419 DPLQARQTYAYGTQHDYFDHHDIIIGWTRGSDSSHNSGSLATIMSDPGGNKMYVGRKH 478
Qy      478 AGQWRDITGNRSQVITINADGWNFTNGCAVSVMV 514
Db      479 AGQWRDITGNRSQVITINADGWNFTNGCAVSVMV 515

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RESULT 6

```

A1BSN
alpha-amyase (EC 3.2.1.1) precursor - Bacillus amyloliquefaciens
N/Alternate names: 1,4-alpha-D-glucan glucanohydrolase
C/Species: Bacillus amyloliquefaciens
C/Date: 30-Nov-1980 #sequence_revision 30-Jun-1987 #text_change 16-Aug-2004
C/Accession: A92389; A90307; I39756; I39756; A00643
R/Takkinen, K.; Petersson, R.F.; Kalkkinen, N.; Palva, I.; Soderlund, H.; Kaariainen, L.
J. Biol. Chem. 258, 1007-1013, 1983
A/Title: Amino acid sequence of alpha-amyase from Bacillus amyloliquefaciens deduced fr
A/Reference number: A92389; MUID:83108808; PMID:6185474
A/Contents: PUB110
A/Accession: A92389
A/Molecule type: DNA
A/Residues: 1-514 <TAX>
A/Cross-references: UNIPROT:P00692; GB:J01542; GB:J01543; GB:M12033; GB:M12034; NID:g1424
R/Chung, H.S.; Friedberg, F.
Biochem. J. 185, 387-395, 1980
A/Title: Sequence of the N-terminal half of Bacillus amyloliquefaciens alpha-amyase.
A/Reference number: A90307; MUID:802411725; PMID:6156671
A/Accession: A90307
A/Molecule type: protein
A/Residues: 32-53, 'I', '55-63, 'L', '65-78, 'D', '80-83, 'S', '85-222 <CHD>
R/Palva, I.; Petersson, R.F.; Kalkkinen, N.; Lehtovaara, P.; Sarvas, M.; Soderlund, H.;
Gene 15, 43-51, 1981
A/Title: Nucleotide sequence of the promoter and NH2-terminal signal peptide region of t
A/Reference number: I39756; MUID:82051296; PMID:6170539
A/Accession: I39756
A/Status: translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-96 <RES>
A/Cross-references: EMBL:V00092; NID:g39297; PIDN:CAA23430.1; PID:g39298
R/Ruohonen, L.; Hackman, P.; Lehtovaara, P.; Knowles, J.K.C.; Karainen, S.
Gene 59, 161-170, 1987
A/Title: Efficient secretion of Bacillus amyloliquefaciens alpha-amyase cells by its ovr
A/Reference number: I39763; MUID:88137952; PMID:2830166
A/Accession: I39763
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-39 <RE2>
A/Cross-references: GB:M18424; NID:g142430; PIDN:AAA22192.1; PID:g142431

```


C/Function: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
 A/Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
 A/Pathway: glycoen/starch degradation
 C/Superfamily: Alpha-amylase, amylolicefens type; alpha-amylase core homology
 C/Keywords: extracellular protein; glycosidase; hydrolase; polysaccharide degradation
 F:1-31/Domains: signal sequence #status predicted <SIG>
 F:32-514/Product: alpha-amylase #status predicted <MPT>
 F:129-362/Domains: alpha-amylase core homology <AMY>
 F:133,231,266/Binding site: calcium (Asn, Asp, His) #status predicted
 F:262,292,359/Active site: Asp, Glu, Asp #status predicted

Query Match 64.5%; Score 1845.5; DB 1; Length 514;
 Best Local Similarity 63.8%; Pred. No. 7.2e-118;
 Matches 329; Conservative 74; Mismatches 100; Indels 13; Gaps 4;

```

QY 6 RIISLTLTLLAVLPPYMTPEPAQHNGNTMMQYFEMHLIPDNGHNRRLDPAANL 65
DB 7 RIVSRRLVLMCTLFLVSPITKT---SAVGTLMQYFEMVTPNDGQHWKRLDPAANL 61
QY 66 KSKGTTAVWIPPAWKGTSQNDVGYAYDLVLDGEFNGQVTRTKYTSQLOAGATSLKN 125
DB 62 SDIGTTAVWIPPAWKGTSQNDVGYAYDLVLDGEFNGQVTRTKYTSQLOAGATSLKN 121
QY 126 NGIYGVGVVNAHKGADGTEWVNAEVRNSNRNOISGEYTIEMTKYFDPFGNGTSHN 185
DB 122 RNVQYGVGVVNAHKGADGTEWVNAEVRNSNRNOISGEYTIEMTKYFDPFGNGTSHN 181
QY 186 FKMWHYHEDGTDPMOSROLOKIKYKRGTKAMPEVNIENGNDYLYMAADIMDHEVI 245
DB 182 FKMWHYHEDGTDPMOSROLOKIKYKRGTKAMPEVNIENGNDYLYMAADIMDHEVI 240
QY 246 NELNMGVWYNTNLNDGFRIDAVGHIKYSYTRDMLTVRMTGKPMFAVAFKMDLAA 305
DB 241 AETKMGWYANLSDIFRIDAAGHIKFSFLRDMVQAVROATGEMTVAEYQNNMGK 300
QY 306 IENTYKTSWNSHVFDPVPLHYNLYNASNGYFDMRNILNGSVQKPIHATVPNDHS 365
DB 301 LENTYKTSWNSHVFDPVPLHYNLYNASNGYFDMRNILNGSVQKPIHATVPNDHS 360
QY 366 OPGFALSFVQSWFPELAVALLITREOGYPSVFQDYGIPTHG-----VSMKSKIDL 420
DB 361 OPGFALSFVQSWFPELAVALLITREOGYPSVFQDYGIPTHG-----VSMKSKIDL 418
QY 421 LQAGTYAVGTQHDYFDHDIIGWTRBGSSHPNSGLATIMSDGPGKMYVYGKHAQO 480
DB 419 LKAKKEYAVGPQHDYIDHDIIGWTRBGSSHPNSGLATIMSDGPGKMYVYGKHAQO 478
QY 481 VWRDITGNRSGVTITNDGWNFTVNGAVSWVWQ 516
DB 479 TWYDITGNRSDTVIKISDGWGEFHNDSVSIVYQK 514

```

RESULT 7

ALBSE
 alpha-amylase (EC 3.2.1.1) precursor - *Bacillus stearothermophilus* (strain DY-5) plasmid

N/Alternate names: 1,4-alpha-D-glucan glucanohydrolase
 C/Species: *Bacillus stearothermophilus*
 C/Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 16-Aug-2004
 C/Accession: A91999; B91999; A00845
 J/Ihara, H.; Sasaki, T.; Tsuboi, A.; Yamagata, H.; Tsukagoshi, N.; Uda, S.
 J. Biochem. 98, 95-103, 1985
 A/Title: Complete nucleotide sequence of a thermophilic alpha-amylase gene: homology bet
 A/Reference number: A91999; MUID:86008166; PMID:3876333
 A/Accession: A91999
 A/Molecule type: DNA
 A/Residues: 1-548 <1H>
 A/Cross-references: UNIPROT:P06279; GB:X02769
 A/Experimental source: plasmid PH100 from strain DY-5
 A/Accession: B91999
 A/Molecule type: protein
 A/Residues: 35-48 <1H>
 A/Experimental source: strain DY-5
 R/Tsukagoshi, N.; Ihara, S.; Sasaki, T.; Takemura, T.; Ihara, H.; Idota, Y.; Yamagata,

J. Bacteriol. 164, 1182-1187, 1985
 A/Title: Efficient synthesis and secretion of a thermophilic alpha-amylase by protein-pr
 A/Reference number: A91804; MUID:86059211; PMID:2999073

A/Contents: pBAM101
 A/Accession: A91804
 A/Molecule type: DNA
 A/Residues: 1-29, 'Q', 31-75, 'W', 77-122 <TSU>
 A/Comment: Alpha-amylase genes have been found on plasmids and in multiple copies on the
 C/Genetics:
 A/Genome: plasmid
 A/Start codon: GTG

C/Function: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
 A/Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
 A/Pathway: glycoen/starch degradation
 C/Superfamily: Alpha-amylase, amylolicefens type; alpha-amylase core homology
 C/Keywords: extracellular protein; glycosidase; heat-stable protein; hydrolase; polysac
 F:1-34/Domains: signal sequence #status predicted <SIG>
 F:35-548/Product: alpha-amylase #status experimental <MAT>
 F:235-368/Domains: alpha-amylase core homology <AMY>
 F:139,237,272/Binding site: calcium (Asp, Asp, His) #status predicted
 F:268,298,365/Active site: Asp, Glu, Asp #status predicted

Query Match 64.2%; Score 1837; DB 1; Length 548;
 Best Local Similarity 63.7%; Pred. No. 3e-117;
 Matches 331; Conservative 71; Mismatches 106; Indels 12; Gaps 5;

```

QY 1 MKNRIIS---VLTLLAVLPPYMTPEPAQHNGT---NGTMMQYFEMHLIPDNGH 54
DB 1 MKNRIIS---VLTLLAVLPPYMTPEPAQHNGT---NGTMMQYFEMHLIPDNGH 56
QY 55 WNRLLDDAANLKSIGITAWIPPAWKGTSQNDVGYAYDLVLDGEFNGQVTRTKYTSQ 114
DB 57 WTKYANENNNLSIGITAWIPPAWKGTSQNDVGYAYDLVLDGEFNGQVTRTKYTSQ 116
QY 115 QLOAGVTSLSKNGIGIYGVGVVNAHKGADGTEWVNAEVRNSNRNOISGEYTIEMTK 174
DB 117 QYLOAGVTSLSKNGIGIYGVGVVNAHKGADGTEWVNAEVRNSNRNOISGEYTIEMTK 176
QY 175 DPGFGNTSHNFKRWYHFDGTDPMOSROLOKIKYKRGTKAMPEVNIENGNDYLYMA 234
DB 177 DPGFGNTSHNFKRWYHFDGTDPMOSROLOKIKYKRGTKAMPEVNIENGNDYLYMA 235
QY 235 ADIMDHEVNIENLNNGWYNTNLNDGFRIDAVGHIKYSYTRDMLTVRMTGKPMFA 294
DB 236 ADIMDHEVNIENLNNGWYNTNLNDGFRIDAVGHIKYSYTRDMLTVRMTGKPMFA 295
QY 295 VAEFWKNDLAIENYLNKTSWNSHVFDPVPLHYNLYNASNGYFDMRNILNGSVQKPI 354
DB 296 VAEFWKNDLAIENYLNKTSWNSHVFDPVPLHYNLYNASNGYFDMRNILNGSVQKPI 355
QY 355 HATFVNDHDSQPEALSFVQSWFPELAVALLITREOGYPSVFQDYGIPTHGVS 414
DB 356 HATFVNDHDSQPEALSFVQSWFPELAVALLITREOGYPSVFQDYGIPTHGVS 414
QY 415 SKIDPLQAGTYAVGTQHDYFDHDIIGWTRBGSSHPNSGLATIMSDGPGKMYVYG 474
DB 415 SKIDPLQAGTYAVGTQHDYFDHDIIGWTRBGSSHPNSGLATIMSDGPGKMYVYG 474
QY 475 KHAQGVWYRDITGNRSGVTITNDGWNFTVNGAVSWVW 514
DB 475 KHAQGVWYRDITGNRSGVTITNDGWNFTVNGAVSWVW 514

```

RESULT 8

alpha-amylase (EC 3.2.1.1) - *Bacillus circulans*

C/Species: *Bacillus circulans*
 C/Date: 18-Feb-1984 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
 C/Accession: S15713
 R/Marcel, T.
 submitted to the EMBL Data Library, May 1991
 A/Reference number: S15713
 A/Accession: S15713

A:Molecule type: DNA
 A:Residues: 1-493 <MAR>
 A:Cross-references: UNIPROT:Q03657; EMBL:X60779; NID:g39411; PIDN:CAA3194.1; PID:g39412
 C:Genetics:
 A:Gene: amyE
 C:Function:
 A:Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
 A:Pathway: glycogen/starch degradation
 C:Superfamily: alpha-amyase, amyloliquefaciens type; alpha-amyase core homology
 C:Keywords: glycosidase; hydrolase; polysaccharide degradation
 F:200-333/Domain: alpha-amyase core homology <AMY>

Query Match 47.1%; Score 1347; DB 2; Length 493;
 Best Local Similarity 51.4%; Pred. No. 5.1e-84;
 Matches 247; Conservative 73; Mismatches 153; Indels 8; Gaps 3;

```

QY 37 NGTMMQYFEMHLPNDGNHNRRLRDAANLKSIGITAWIPPAWKGTSQNDVGYGAYDLYD 96
DB 4 NHTMMQFEFHTLADGDHMKRLAEMAPELKAKGIDTWVPVTKAVASAEITGYGVYDLYD 63
QY 97 LGFENQKGVTRTKYKTRSQLGAVTSLKNGIIOYGVVNNHKGADGTEMNAVEVNS 156
DB 64 LGFEDQKGVTRTKYKTRSQLGAVTSLKNGIIOYGVVNNHKGADGTEMNAVEVNS 123
QY 157 NNRQETSGEYTTIEMTKEDPGRGNTHSNFKRMWYHEDGTMDQSRLOKIKYKPGTGK 216
DB 124 DRKTEISEPPELGWTKFTPGRGDOYSFKMNSHEHNGTDFD-AREERTGVRIAGENK 182
QY 217 AMDMEVDIENGNYDYLMYADIDMDHPEVINELRNWGVYNTNTLNDGFRIDAVKHIKYSY 276
DB 183 KMNENVDDEFNGDYLMFAIDYNHNPVREMIIDWGMKILDTLQCGGFRIDALIKHINHER 242
QY 277 TRDMLTHVRNTTGKPMFAVAEPKNDLAIENYLNKTSNMHSVPDPLAHNLNNAASNG 336
DB 243 IKFAEMIKRQODFYIABEPMNSNLDACREPLDTYQIDLEFVSLHKKHBAKGR 302
QY 337 YFMRNLINGSVQKHPHIAVTVDNHDSDGSEALSEFVQSWKPLAYALILTRGQYPS 396
DB 303 DFDLSKIFDITVOTHTHVAVTVDNHDSDGSEALSEFVQSWKPLAYALILTRGQYPS 362
QY 397 VFYGDYGI-----PTHGVPMSKSIDPLLOARQTYAGTGHDPYDHHDIIGWTREDDSSH 452
DB 363 VFYGDYGIAGPEFVDG---KKEILDITLISARCNKAGGEDEYFDHANTIGWRGVEEI 419
QY 453 PNGSLATINDGPGGNKMTYVGGKAKGQVWRDITGNRSGVTINADGWNFTYNGAVSY 512
DB 420 EGGSCAAVVISGNDGKRMFIDGEHAGEVWVDLTRSCDDITLEDGMATFHVCGGGSV 479
QY 513 W 513
DB 480 W 480

```

RESULT 9

alpha-amyase [imported] - Streptococcus pneumoniae (strain TIGR4)
 C:Species: Streptococcus pneumoniae
 C>Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 09-Jul-2004
 C:Accession: G95160
 R:Retelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Held
 on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzaple,
 nson, T.; Hickey, E.K.; Holt, I.E.
 Science 293, 498-506, 2001
 A:Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison,
 A:Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.
 A:Reference number: A95000; MUID:21357209; PMID:11463916
 A:Accession: G95160
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-484 <KUR>
 A:Cross-references: UNIPROT:Q97049; GB:AE005672; PIDN:AAK75480.1; PID:g14972868; GSPDB:C
 C:Experimental source: strain TIGR4
 C:Genetics:

A:Gene: SPI382
 C:Superfamily: alpha-amyase, amyloliquefaciens type; alpha-amyase core homology
 Query Match 43.3%; Score 1240; DB 2; Length 484;
 Best Local Similarity 48.8%; Pred. No. 9.4e-77;
 Matches 234; Conservative 74; Mismatches 166; Indels 6; Gaps 4;

```

QY 37 NGTMMQYFEMHLPNDGNHNRRLRDAANLKSIGITAWIPPAWKGTSQNDVGYGAYDLYD 96
DB 3 NHTMMQFEFHTLADGDHMKRLAEMAPELKAKGIDTWVPVTKAVASAEITGYGVYDLYD 62
QY 97 LGFENQKGVTRTKYKTRSQLGAVTSLKNGIIOYGVVNNHKGADGTEMNAVEVNS 156
DB 64 LGFEDQKGVTRTKYKTRSQLGAVTSLKNGIIOYGVVNNHKGADGTEMNAVEVNS 122
QY 157 NNRQETSGEYTTIEMTKEDPGRGNTHSNFKRMWYHEDGTMDQSRLOKIKYKPGTGK 216
DB 123 DRTVELGSEPTINGTSTFEDGRDPTVNGFHHWHFTGTDYDKRS-KSGITLQGDYK 181
QY 217 AMDME--VDIENGNYDYLMYADIDMDHPEVINELRNWGVYNTNTLNDGFRIDAVKHIKYSY 274
DB 182 GWANBELVINGENYDYLMYADIDDFGHPREVIONITMDMFMETTSVAGFRIDAVKHIDS 241
QY 275 SYTRDMLTHVRNTTGKPMFAVAEPKNDLAIENYLNKTSNMHSVPDPLAHNLNNAASNS 334
DB 242 FFWBNFIRMKKEYGDDFVPGEFNNPDKEANLIDYEKTEEHFDLYDVRHLQNLFEASQA 301
QY 335 GGYFMRNLINGSVQKHPHIAVTVDNHDSDGSEALSEFVQSWKPLAYALILTRGQYPS 394
DB 302 GANYDILRGIFETSLVELKDKKAVTFPDNDHTDYGQALBSTVEWEPFAVYALILTRQDEL 361
QY 395 PSYFVGDIYGIPT-THGVPMSKSIDPLLOARQTYAGTGHDPYDHHDIIGWTREDDSSH 453
DB 362 PCVFYDIDYIGISQVYAEQEPKILDLRLAIRDLYAGEONDYFDHANCIGWRSG--AAN 419
QY 454 NSGLATINDGPGGNKMTYVGGKAKGQVWRDITGNRSGVTINADGWNFTYNGAVSY 513
DB 420 QSPIAVLISNDQNSKSMFVGEWETQTQFVDLIGNHQGVITIDEEGQGPVSARSVSVM 479

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RESULT 10

alpha-amyase [imported] - Nostoc sp. (strain PCC 7120)
 C:Species: Nostoc sp. PCC 7120
 A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
 C>Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 16-Aug-2004
 C:Accession: AH2079
 R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi,
 Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Tabata, S.
 DNA Res. 8, 205-213, 2001
 A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anab
 A:Reference number: AB1807; MUID:21595285; PMID:11759840
 A:Accession: AH2079
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-492 <KUR>
 A:Cross-references: UNIPROT:Q8YU21; GB:BA000019; PIDN:BBB73689.1; PID:g17131281; GSPDB:G
 A:Experimental source: strain PCC 7120
 C:Genetics:
 A:Superfamily: Alpha-amyase, amyloliquefaciens type; alpha-amyase core homology

Query Match 43.3%; Score 1240; DB 2; Length 492;
 Best Local Similarity 48.4%; Pred. No. 9.6e-77;
 Matches 238; Conservative 79; Mismatches 157; Indels 18; Gaps 6;

```

QY 37 NGTMMQYFEMHLPNDGNHNRRLRDAANLKSIGITAWIPPAWKGTSQNDVGYGAYDLY 95
DB 5 NHTMMQYFEMHLPNDGNHNRRLRDAANLKSIGITAWIPPAWKGTSQNDVGYGAYDLY 64
QY 96 DLGEPQKGVTRTKYKTRSQLGAVTSLKNGIIOYGVVNNHKGADGTEMNAVEVNS 155
DB 65 DLGEPQKGVTRTKYKTRSQLGAVTSLKNGIIOYGVVNNHKGADGTEMNAVEVNS 124

```

QY 156 SNNQISGEYTIEMTKEDPFGKNTSHNFKRWYHFDGTDMDQ-SRQLONKIKYKFGT 214
 Db 125 DDLRLPKGLDIDIKYTYTTFPGKNTSHNFKRWYHFDGTDMDQ-SRQLONKIKYKFGT 182
 QY 215 GKAMDVEVDIENGNYDLYADIDMDHPEVINELRNMGWYTNLTLDGFRIDAVKHIXY 274
 Db 183 GKNFDYVALEKGNFAYILMGCDLDFQNEWVGEVITYWGMGCLDTKXGDFRIDALIKHIST 242
 QY 275 SYTRDMLTHVANTTKGPMFAVAEFKNDLAIENYLNKTSNMNSHFPDYLPHNYLNASNS 334
 Db 243 WFFPEWIDALERRHAGKOLFVWGEVYVNDINTLWYVDVAVRGMSVFDVPLHNFQOAKS 302
 QY 335 GGFYEMRIILNGSVYQKPHIAVTFVNDHSDQPGFALBSFYQSWFKPLAYALILTRREGY 394
 Db 303 GGNIDMRILIDGTGMQKQPHIAVTFVNDHSDQPGFALBSFYQSWFKPLAYALILTRREGY 362
 QY 395 PSVFYGDYGGIPTHG-----VPSMSKIDPLLOARQTYAGTQHDYFDHHDILG 443
 Db 363 PCVFHADYGAAYEDMGKGNRYNIFMSHRIIDKLAYARKHYVGPQYVLDHMTIG 422
 QY 444 WTRBDSHSHNSGLATINSDDPGKKNMYVGHKAGQVWRDITGNRSCTVTIINADGKGF 503
 Db 423 WTRIGDADHP-QGMAVIMSDSEGIKMEVGKPTKFI--DLTEHKEAVYTNEWGWGEF 479
 QY 504 TVNGGAVSVWYK 515
 Db 480 RCLGGSVSVWVQ 491

RESULT 11

F98026
 alpha-amylase (EC 3.2.1.1) precursor [imported] - Streptococcus pneumoniae (strain R6)
 C:Species: Streptococcus pneumoniae
 C:Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 16-Aug-2004
 C:Accession: F98026
 R:Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszcak, L.; Burgett, S.; DeHoff, B.S.; E
 y, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAnnen, S.; M
 y, P.; Sun, P.M.; Winkler, M.E.
 J. Bacteriol. 183, 5709-5717, 2001
 A:Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.;
 A:Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.
 A:Reference number: A97872; MUID:21429245; PMID:11544234
 A:Accession: F98026
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-484 <KUR>
 A:Cross-references: UNIPROT:Q8DPC8; GB:AE007317; PIDN:AAL00043.1; PID:g15458876; GSPDB:C
 C:Genetics:
 A:Gene: amy
 C:Superfamily: Alpha-amylase, amyloliquefaciens type; alpha-amylase core homology
 C:Keywords: glycosidase; hydrolase

Query Match 43.3%; Score 1238; DB 2; Length 484;
 Best Local Similarity 48.5%; Pred. No. 1.3e-76;
 Matches 233; Conservative 76; Mismatches 165; Indels 6; Gaps 4;
 QY 37 NGTMOYFEMHLPNDDGNHNRFLRDDANLKSIGITAVWIPPAWKSTSONDVGAYDYLD 96
 Db 3 NOTMOYFEMWLPDGGQHTRLAENAPHLAHLGISHWMPAPAFATNEKDVGYGVYDFD 62
 QY 97 LGFENOGKVTATKYGTSQLOCAVTSLKNGIQQYGVVNMHKGAGDTEWNAVEVNR 156
 Db 63 LGFENOGKVTATKYGTSQLOCAVTSLKNGIQQYGVVNMHKGAGDTEWNAVEVNR 122
 QY 157 NNRQISGEYTIEMTKEDPFGKNTSHNFKRWYHFDGTDMDQSRQLONKIKYKFGTK 216
 Db 123 DRYTELGPFTINGSTFTPDGRQDTYGFHMHYHFTGTDYDAKRS-KSGIYLILQGNK 181
 QY 217 AWDME--VDIENGNYDIYADIDMDHPEVINELRNMGWYTNLTLDGFRIDAVKHIXY 274
 Db 182 GMAVEELVDNENGVYDLYADIDMDHPEVINELRNMGWYTNLTLDGFRIDAVKHIDS 241

QY 275 SYTRDMLTHVANTTKGPMFAVAEFKNDLAIENYLNKTSNMNSHFPDYLPHNYLNASNS 334
 Db 242 FPNRNFIDMEKXGDDPYVGEFNSKXANLIDLETBEHFDLVDRHLQNLFEASQA 301
 QY 335 GGFYEMRIILNGSVYQKPHIAVTFVNDHSDQPGFALBSFYQSWFKPLAYALILTRREGY 394
 Db 302 GANYDLRGIPTDLSVLEKPKAVTFVNDHSDQPGFALBSFYQSWFKPLAYALILTRREGY 361
 QY 395 PSVFYGDYGGIP-THGVSMSKIDPLLOARQTYAGTQHDYFDHHDILG 443
 Db 362 PCVFHADYGAAYEDMGKGNRYNIFMSHRIIDKLAYARKHYVGPQYVLDHMTIG 422
 QY 444 WTRBDSHSHNSGLATINSDDPGKKNMYVGHKAGQVWRDITGNRSCTVTIINADGKGF 503
 Db 420 QSPILAVLISNDESKSMFVQGEWNTQTFVLDLASHQGVYTIIDEGIGQFVVSARSVW 479

RESULT 12

C66781
 alpha-amylase [imported] - Lactococcus lactis subsp. lactis (strain IL1403)
 C:Species: Lactococcus lactis subsp. lactis
 C:Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 16-Aug-2004
 C:Accession: C66781
 R:Boletín, A.; Winkler, P.; Manger, S.; Jallón, O.; Malarme, K.; Weisenbach, J.; Ehrli,
 Genome Res. 11, 731-753, 2001
 A:Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis
 A:Reference number: A66625; MUID:21235186; PMID:11337471
 A:Accession: C66781
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-491 <STO>
 A:Cross-references: UNIPROT:Q9GCS9; GB:AE005176; PID:g12724224; PIDN:AAK05349.1; GSPDB:C
 A:Experimental source: Strain IL1403
 A:Genetics:
 C:Superfamily: Alpha-amylase, amyloliquefaciens type; alpha-amylase core homology

Query Match 39.6%; Score 1133; DB 2; Length 491;
 Best Local Similarity 43.0%; Pred. No. 1.8e-69;
 Matches 205; Conservative 96; Mismatches 172; Indels 4; Gaps 3;
 QY 39 TMOYFEMHLPNDDGNHNRFLRDDANLKSIGITAVWIPPAWKSTSONDVGAYDYLD 97
 Db 3 TMOYFEMHLPNDDGNHNRFLRDDANLKSIGITAVWIPPAWKSTSONDVGAYDYLD 62
 QY 98 GFENOGKVTATKYGTSQLOCAVTSLKNGIQQYGVVNMHKGAGDTEWNAVEVNR 157
 Db 63 GFENOGKVTATKYGTSQLOCAVTSLKNGIQQYGVVNMHKGAGDTEWNAVEVNR 122
 QY 158 NNRQISGEYTIEMTKEDPFGKNTSHNFKRWYHFDGTDMDQSRQLONKIKYKFGTK 217
 Db 123 HAHNIENKVTATKYGTSQLOCAVTSLKNGIQQYGVVNMHKGAGDTEWNAVEVNR 179
 QY 218 WMEVDIENGNYDLYADIDMDHPEVINELRNMGWYTNLTLDGFRIDAVKHIXY 277
 Db 180 WMEVDIENGNYDLYADIDMDHPEVINELRNMGWYTNLTLDGFRIDAVKHIXY 239
 QY 278 RDMLTAVRANTTKGPMFAVAEFKNDLAIENYLNKTSNMNSHFPDYLPHNYLNASNGY 337
 Db 240 RDMLTAVRANTTKGPMFAVAEFKNDLAIENYLNKTSNMNSHFPDYLPHNYLNASNGY 299
 QY 338 FDMENILNGSVYQKPHIAVTFVNDHSDQPGFALBSFYQSWFKPLAYALILTRREGY 397
 Db 300 FDMENILNGSVYQKPHIAVTFVNDHSDQPGFALBSFYQSWFKPLAYALILTRREGY 359
 QY 398 PSVFYGDYGGIP-THGVSMSKIDPLLOARQTYAGTQHDYFDHHDILG 443
 Db 360 PSVFYGDYGGIP-THGVSMSKIDPLLOARQTYAGTQHDYFDHHDILG 419
 QY 444 WTRBDSHSHNSGLATINSDDPGKKNMYVGHKAGQVWRDITGNRSCTVTIINADGKGF 503
 Db 420 WTRBDSHSHNSGLATINSDDPGKKNMYVGHKAGQVWRDITGNRSCTVTIINADGKGF 476

RESULT 13

G98247

Cyttoplasmic alpha-amylase (1,4-alpha-D-glucan glucanohydrolase) [Imported] - Agrobacterium tumefaciens

C/Species: Agrobacterium tumefaciens

C/Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004

C/Accession: G98247

R/Gooder, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Quirillo, B.; Goldman, A.; Liu, F.; Wollam, C.; Allinger, M.; Dougherty, D.; Scott, C.; Lappas, C.; Markelz, B.; Science 294, 2323-2328, 2001

A/Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tumefaciens

A/Reference number: A97359; MUID:21608551; PMID:11743194

A/Accession: G98247

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-506 <KUR>

A/Cross-references: UNIPROT:Q8U916; GB:AE007870; PID:AAK89505.1; PID:g15159379; GSPDB:G

A/Genetic: AGR_L_1863

A/Map position: linear chromosome

C/Superfamily: alpha-amylase, amy101iquefaciens type; alpha-amylase core homology

Query Match 38.1%; Score 1090.5; DB 2; Length 506;

Best Local Similarity 44.3%; Pred. No. 1.4e-66;

Matches 224; Conservative 80; Mismatches 181; Indels 21; Gaps 9;

25 MTEPAQAHNG--TNGTMQYFEWHLFNDGNHNRRLDDAANKSKGITAVMIPPAWKT 82

1 MARPAN-HREGNMGARITLQFFHWYDPDGKLMSEVAKESLAKMGITDVMLEPAWKA 59

83 SQN-DVGYGAYDLYDLGFENQKGYRTKGYRSLQAGAVTSLKNGIQVYGDVVMNKKG 141

60 AGGVSQVYDYDDYDLGFENQKGYRTKGYRSLQAGAVTSLKNGIQVYGDVVMNKKG 119

142 ADGTEWNAVEVNRNSNNOEISGEYTEATKEDPGRGNTHSNFKRMWHPDGTWDS 201

120 ADEKRYKRVNRPDDTDIDDEPRLATRTFFPRNKGHSKFIMDLKCFSGVDHIE- 178

202 ROLNKKYK--RGTGKAMDEVDIENGNDYIMVADIDMDHEVINELRNMGWYTNLT 258

179 EPTEDGIFRLVNEYGDE--WNEEVDQENGFEDYLMGADVEFRNRAVVEELKYGWMLSEQ 237

259 LINDGFRLDAVKHLYSYTDMVLTGKMPFAVAEFKNDIALENYLNTKSNHNS 318

238 VQVDFGLDAKHLPANFPRDWGMRKRYDPLFVVAEYVHPDLKSYELVDKQLM 297

319 VFDPVLYNLYNANSGGYFDMRNILNGSVVQKAPHAVTFVNDHSQPEALSFVQSW 378

298 LFDVALHHSFHDASKOGGDFMRSIFPGSLSAVPRDAVTLVDNHDTPQLQSLAEPV 357

379 FKPLAYALLTRGQYGVYFGDYG--IPTHGVPMSKSID-----PLQARQTYA 428

358 FKPLAYAILLREBQVPCVFPYDLEFGSYDTGNDGNEYKIDIPALECLPRLIARERFA 417

429 YGTQHDVDFDHDIIIGMTREDSHPNSGLATIMSDGPGKMMYVGGKXAGQVMDITGN 488

418 NGPOTDIFDDASCIATFIRHGTADAP--GCVVVMNGBERGKQADLGPBRASVWRDPLGH 475

489 RSGVTITNADGMGNTVNGAVSVWV 514

476 REEHITLDESCKGFFPTNGSGSVSWV 501

RESULT 14

AD3038

alpha-amylase amya [Imported] - Agrobacterium tumefaciens (strain C58, Dupont)

C/Species: Agrobacterium tumefaciens

C/Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 16-Aug-2004

C/Accession: AD3038

R/Gooder, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Quirillo, B.; Goldman, A.; Liu, F.; Wollam, C.; Allinger, M.; Dougherty, D.; Scott, C.; Lappas, C.; Markelz, B.; Science 294, 2323-2328, 2001

A/Reference number: A97359; MUID:21608551; PMID:11743194

A/Accession: AD3038

A/Status: preliminary

A/Molecule type: DNA

A/Cross-references: UNIPROT:Q8U916; GB:AE007870; PID:AAK89505.1; PID:g15159379; GSPDB:G

A/Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, J. S.; E.W.

A/Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.

A/Reference number: A42577; MUID:21608550; PMID:11743193

A/Accession: AD3038

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-495 <KUR>

A/Cross-references: UNIPROT:Q8U916; GB:AE008669; PID:AA44722.1; PID:g17742354; GSPDB:G

A/Experimental source: strain C58 (Dupont)

A/Genetic: amya

A/Map position: linear chromosome

C/Superfamily: Alpha-amylase, amy101iquefaciens type; alpha-amylase core homology

Query Match 37.9%; Score 1084; DB 2; Length 495;

Best Local Similarity 44.7%; Pred. No. 3.9e-66;

Matches 219; Conservative 80; Mismatches 173; Indels 18; Gaps 7;

39 TMQYFEWHLFNDGNHNRRLDDAANKSKGITAVMIPPAWKTSON-DVGYGAYDLYDL 97

5 TLLQFFHWYDPDGKLMSEVAKESLAKMGITDVMLEPAWKAAGVSGVDTYDLDL 64

98 GFENQKGYRTKGYRSLQAGAVTSLKNGIQVYGDVVMNKKGADGTEWNAVEVNRNS 157

65 GFEDQKGYATKGYRSLQAGAVTSLKNGIQVYGDVVMNKKGADGTEWNAVEVNRNS 124

158 KNOEISGEYTEATKEDPGRGNTHSNFKRMWHPDGTWDSQOLNKKYK--RGT 214

125 RTDIDEDPRLATRTFFPRNKGHSKFIMDLKCFSGVDHIE-BPTEDGIFRLVNEYG 183

215 GRAMDEVDIENGNDYIMVADIDMDHEVINELRNMGWYTNLTNLDGFRIDAVKIKY 274

184 GE-WNEEVDQENGFEDYLMGADVEFRNRAVVEELKYGWMLSEQVQVDFGLDAKHIPA 242

275 SYTRDMLFVNRITGKMPFAVAEFKNDIALENYLNTKSNHNSVFPDVLNLYNANSG 334

243 WFRDVGMRKRYDPLFVVAEYVHPDLKSYELVDKQLMFLDVALHHSFHDASKQ 302

335 GGYFDMRNILNGSVVQKAPHAVTFVNDHSQPEALSFVQSWFKPLAYALLTRGQY 394

303 GGFDMRSIFPGSLSAVPRDAVTLVDNHDTPQLQSLAEPVFKPLAYAILLREBQV 362

395 PSVFGDYG--IPTHGVPMSKSID-----PLQARQTYAVGTQHDVDFDHDIIIGW 444

363 PCVFPYDLEFGSYDTGNDGNEYKIDIPALECLPRLIARERFAVPRDAVTLVDNHDTPQLQSLAEPV 422

445 TREGDSHPNSGLATIMSDGPGKMMYVGGKXAGQVMDITGNNSGVTITNADGMGNT 504

423 IRHGTADAP--GCVVVMNGBERGKQADLGPBRASVWRDPLGHREHITLDESCKGTFP 480

505 VNGGAVSVWV 514

481 TNGGAVSVWV 490

RESULT 15

B45738

alpha-amylase (EC 3.2.1.1), cytosolic - Salmonella typhimurium

N/Alternate names: 1,4-alpha-D-glucan glucanohydrolase

C/Species: Salmonella typhimurium

C/Date: 07-Apr-1994 #sequence_revision 18-Aug-1995 #text_change 16-Aug-2004

C/Accession: B45738

R/Raha, M.; Kawagishi, I.; Mueller, V.; Kihara, M.; Macnab, R.M.

J. Bacteriol. 174, 6644-6652, 1992

A/Title: Escherichia coli produces a cytoplasmic alpha-amylase, amya.

A/Reference number: A45738; MUID:93015717; PMID:1400215

A/Accession: B45738

A/Molecule type: DNA

A/Residues: 1-494 <RAH>

A/Cross-references: UNIPROT:P26613; GB:L01643; NID:g154043; PID:AAA27110.1; PID:g154045

C/Genetics:

A/Genetic: amya

C;Function:

A:Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A:Pathway: glycogen/starch degradation

A; Pathway: glycogen/starch degradation

C:Superfamily: alpha-amylase, amylioliquefaciens type, alpha-amylase core homology
C:Keywords: cytosol; glycosidase; hydrolase; polysaccharide degradation

Keywords: cytosol; glycosidase; hydrolase; polysaccharide degradation

F;202-335/Domain: alpha-amylase core homology <AMY>
F;239,265,332/Active site: His, Glu, Asp #status predicted

F:239,265,332/Active site: His, Glu, Asp #status predicted

Query Match	36.8%;	Score 1053;	DE 1;	Length 494;
Best Local Similarity	42.1%;	Pred. No. 4.9e-64;		
Matches 207;	Conservative	84;	Mismatches 183;	Indels 18;
			Gaps	6;

```

0Y 37 NCTMAYEPMHLPNCSNHNRLRBDPAANKSKCITAVMIPPAKGSUN--DYVGAVDLY 95
Db 3 NPTLIQFHEWYIPDGGKLMSELAERADGLNDIGINMWLEPACKGASGGYSVGDITDULF 62
0Y 96 DLGEFNOKGTATYTKYSTRSLOGAVSLKNGGIOVYGDVMMNKGADGTEMNAVEVR 155
Db 63 DLGEFDQKTIATKYGDQRQLTALIDAKNNIAVLDDVYVNHKMGADDEKERIRQVRVQ 122
0Y 156 SNRNOEISGEYTI EAWTKFDPFGRGTHSNFKRWYHFDGTMDWSROLONKIKYRG-- 213
Db 123 DDRQTIDNNIIECEGTRTYTPRPAQOYSNFTIDYHCFSGIDHIEHPD--EDGFKLVNDY 181
0Y 214 TGKAMDWEYDINGNVYDMADIDMDHREVINELNKGWYVNTNTLNDGFRIDAVKHK 273
Db 182 TGDGNNDQDDDEMGNFIDYLMGSEIDFERNNAVTIEIKYMARWVEQTHCGFRIDAVGHP 241
0Y 274 YSYTRDMTLTHVANTTCKPMFAVAEFPKNDLALIENTLAKTSNMHSFDPVRLHNLVNASN 333
Db 242 AMFYEMWEIETHOVAVAPKPLFIAEYVSHVEDKIQTIIDVDGKTMLEFPAQMKFHEASR 301
0Y 334 SGGYFEDMINILNGSVOKRPIHAFTFVDNHDSPGEGALESFYVQSMFKPLATYALITREOG 393
Db 302 OGAEYDMGHIFFGTIVLEADPFHATVILVANHDPRLQALERAPVWPKPLATYALITRENG 361
0Y 394 YPSVFEYDYGIPTH-----GVBSMKSKIDPRLQARQTYAVGTOHDYFDHNDII 442
Db 362 VPSVFYRDLYGASVEDSGENGECRVDMEVILNQDLRLILABRGFAHGIQTLFFDHPNCI 420
0Y 443 GWTRGCDSDHPHSGLATINSDRPGNGKMMYVGNKHAQOYWRDITGNRSGVTITNADGWN 502
Db 421 AFSRSGTEENP--GCVVYVLSNDDEGKTIILLGNVYANKTWRFPSGNRDEYVVTNDGEBAT 478
0Y 503 FTVNGAHSVWV 514
Db 479 FPCNAGSVSWV 490

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Search completed: May 2, 2005, 21:56:41
Job time : 25 secs

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Db 241 HPEVIELNMGWYNTNLNLGDFRIDAYKHITKSTRTDMLTHVTRTKPKMPFAVAFK 300
QY 301 NDLAALIENTYKTSNMHSVFDVPLAHYNLYNASNGYFPMRNILNSGVQKPIHAFTV 360
Db 301 NDLAALIENTYKTSNMHSVFDVPLAHYNLYNASNGYFPMRNILNSGVQKPIHAFTV 360
QY 361 DNHDSPGALBSFVQSWFKPLAYAILTRRQGYPSVFYGDYGIPTTHGVPMSKIDPL 420
Db 361 DNHDSPGALBSFVQSWFKPLAYAILTRRQGYPSVFYGDYGIPTTHGVPMSKIDPL 420
QY 421 LQARQYAYGTQDYPDHDHIIIGTRRQGSHPNSGLATIMSDPGANKMYYGKKAQ 480
Db 421 LQARQYAYGTQDYPDHDHIIIGTRRQGSHPNSGLATIMSDPGANKMYYGKKAQ 480
QY 481 VWRDITGNSGVTINADGNGFTVNGAVSVWVKQ 516
Db 481 VWRDITGNSGVTINADGNGFTVNGAVSVWVKQ 516

RESULT 2
AMT6_BACS7
ID AMT6_BACS7 STANDARD; PRT; 518 AA.
AC P19571;
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Glucan 1,4-alpha-maltohexaosidase precursor (EC 3.2.1.98) (G6-amy1ase)
DE (Maltotetraose-producing amylase) (Exo-maltohexahydrolase).
OS Bacillus sp. (strain 707).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
ON NCBI_TaxID=1416;
RN [1]
RP MEDLINE=88162814; PubMed=3258152;
RA Tsukamoto A., Kimura K., Ishii Y., Takano T., Yamane K.;
RT "Nucleotide sequence of the maltotetraose-producing amylase gene from
RT an alkalophilic Bacillus sp. #707 and structural similarity to
RT 11queyting type alpha-amy1ases."
RL Biochem. Biophys. Res. Commun. 151:25-31(1988).
CC -1- CATALYTIC ACTIVITY: Hydrolysis of 1,4-alpha-D-glucosidic linkages
CC in amylose polysaccharides so as to remove successive
CC maltotetraose residues from the non-reducing chain ends.
CC -1- COFACTOR: Binds 2 calcium ions and 1 sodium ion per subunit (By
CC similarity).
CC -1- PATHWAY: Starch degradation.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the glycosyl hydrolase 13 family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; M18862; AAA22231.1; -.
CC PIR; A27705; A27705.
CC HSSP; P06278; IVTS.
CC DR InterPro; IPR006589; Alp_amy1_cat_sub.
CC DR InterPro; IPR006047; Alpha_amy1_cat.
CC DR InterPro; IPR006046; Glyco_hydro_13.
CC DR Pfam; PF00128; Alpha-amy1ase; 1.
CC DR PRINTS; PR00110; ALPHAMYLASE.
CC DR SMART; SM00642; Amy; 1.
CC KM Carbohydrate metabolism; Direct protein sequencing; Glycosidase;
CC Hydrolyase; Signal.
CC KW SIGNAL 1 33
CC FT CHAIN 34 518 Glucan 1,4-alpha-maltohexaosidase.
CC FT ACT_SITE 269 299 Nucleophile (By similarity).
CC FT ACT_SITE 299 299 Proton donor (By similarity).
CC FT ACT_SITE 366 366 By similarity.

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FT METAL 139 139 Calcium 1 (By similarity).
FT METAL 196 196 Calcium 2 and sodium (By similarity).
FT METAL 219 219 Calcium 2 (via carbonyl oxygen) (By
FT METAL 221 221 similarity).
FT METAL 221 221 Calcium 2 and sodium (By similarity).
FT METAL 232 222 Calcium 1 and sodium (By similarity).
FT METAL 238 238 Calcium 1 and sodium (By similarity).
FT METAL 240 240 Calcium 2 (By similarity).
FT METAL 242 242 Calcium 2 (By similarity).
FT METAL 273 273 Calcium 1 (via carbonyl oxygen) (By
FT METAL 273 273 similarity).
SQ SEQUENCE 518 AA; 59009 MW; 3A961B21612682C4 CRC64;
Query Match 85.2%; Score 2438.5; DB 1; Length 518;
Best Local Similarity 83.7%; Pred. No. 2.6e-156;
Matches 426; Conservative 42; Mismatches 40; Indels 1; Gaps 1;
QY 8 ISVLTLLLAVALPPEYMTTEPAQAHNGNGTMMQYFEWHLEPNDGNHNRDLDAANLKS 67
Db 11 LSLILAFILVITSI-PFTLLVDVEAHNGNGTMMQYFEWHLEPNDGNHNRDLDAANLKS 69
QY 68 KGITAVWIPPAWKGSQNDVGYGAYDLDLGEFPNQKTYRTKYGRSOLQAVTSIKNG 127
Db 70 KGITAVWIPPAWKGSQNDVGYGAYDLDLGEFPNQKTYRTKYGRSOLQAVTSIKNG 129
QY 128 IQYGDVYNNHKGADGTEMNANAVENRSNRNOESGEYTIEMTKFDPGRGNTSNFK 187
Db 130 IQYGVYNNHKGADGTEMNANAVENRSNRNOESGEYTIEMTKFDPGRGNTSNFK 189
QY 188 KRWYHFDGTQDMSROLQNKIKYFRGTGKAMWEVDIENGANYDYADIDMDHEVINE 247
Db 190 KRWYHFDGTQDMSROLQNKIKYFRGTGKAMWEVDIENGANYDYADIDMDHEVINE 249
QY 248 LKNWGWYNTNLNLGDFRIDAYKHITKSTRTDMLTHVTRTKPKMPFAVAFKNDLALE 307
Db 250 LKNWGWYNTNLNLGDFRIDAYKHITKSTRTDMLTHVTRTKPKMPFAVAFKNDLALE 309
QY 308 NYLNTKSNMHSVFDVPLAHYNLYNASNGYFPMRNILNSGVQKPIHAFTVFNHDSOP 367
Db 310 NYLNTKSNMHSVFDVPLAHYNLYNASNGYFPMRNILNSGVQKPIHAFTVFNHDSOP 369
QY 368 GEALBSFVQSWFKPLAYAILTRRQGYPSVFYGDYGIPTTHGVPMSKIDPLQARQY 427
Db 370 GEALBSFVQSWFKPLAYAILTRRQGYPSVFYGDYGIPTTHGVPMSKIDPLQARQY 429
QY 428 AVGTQDYPDHDHIIIGTRRQGSHPNSGLATIMSDPGANKMYYGKKAQWPDITG 487
Db 430 AVGTQDYPDHDHIIIGTRRQGSHPNSGLATIMSDPGANKMYYGKKAQWPDITG 489
QY 488 NRTGVTINADGNGFTVNGAVSVWVKQ 516
Db 490 NRTGVTINADGNGFTVNGAVSVWVKQ 518

RESULT 3
Q59222 PRELIMINARY; PRT; 613 AA.
ID Q59222;
AC Q59222;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Alpha-amy1ase (EC 3.2.2.1).
GN Name=Amy1;
OS Bacillus sp. TS-23.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=38441;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=TS-23;
RA Lin L.-L., Chu W.S., Hsu W.H.;
RL Submitted (MAR-1995) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.
CC EMBL; U22045; AAA63900.1; -.

```


[illegible]

RP SEQUENCE FROM N.A.
 RA Kim Y.B., Lee B.N., Son H.J., Lee J.W., Kim B.J., Kim Y.-W.,
 RA Park K.-H.;
 RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF220440; AAK0598.1; -;
 DR HSSP; P06278; 1VJ5.
 DR GO; GO:0004556; F:alpha-amyase activity; IEA.
 DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
 DR InterPro; IPR006047; Alpha_amy1_cat.
 DR InterPro; IPR006589; Alp_amy1_cat_sub.
 DR Pfam; PF00128; Alpha-amy1ase; 1.
 DR SMART; SM00642; Amy; 1.
 SQ SEQUENCE 533 AA; 60557 MW; 789CECE6A19C7DDE CRC64;

Query Match 68.4%; Score 1957.5; DB 2; Length 533;
 Best Local Similarity 67.7%; Pred. No. 7.5e-124;
 Matches 342; Conservative 60; Mismatches 90; Indels 5; Gaps 3;

QY 16 LAVAVLFPYMTPEPAQAHNG-TNGTMMQYFEMHLPNDGNHNRRLRDAANLKSQGITAVW 74
 DB 30 LSVVMEFLPSIYGSKAYADTVNNGTLMQYFEWYAPNDGNHNRRLRDAENLQKIGITSW 89
 QY 75 IPPAMKTSQNDVGYGAYDLIDLGEFNQKGTVRTKGTSGQLQCAVTSLKNGIQYVGV 134
 DB 90 IPPAYKGTQNDVGYGAYDLIDLGEFNQKGTVRTKGTSGQLQCAVTSLKNGIQYVGV 149
 QY 135 VNMHKGADGTEWNAVEVNRNSNRNOISGEYTIEMTKEDPFGRGNTSHFKRWYHPD 194
 DB 150 VNMHKGADGTEWNAVEVNRNSNRNOISGEYTIEMTKEDPFGRGNTSHFKRWYHPD 209
 QY 195 GTDMDSROLQNKIKYFRGTGKAMDEVDLENGNYDLYADIDMDHPEVINELRWGW 254
 DB 210 GTDMDSROLQNKIKYFRGTGKAMDEVDLENGNYDLYADIDMDHPEVINELRWGW 268
 QY 255 YNTNLMDGFRIDAVYKIKSYTRDMLTHVRNTTGPMPFAVAFWKNDLAIENYLNKTS 314
 DB 269 YANELMDGFRIDAVYKIKSYTRDMLTHVRNTTGPMPFAVAFWKNDLAIENYLNKTS 328
 QY 315 MNHSVDFVPLHYNLVNASNGYFDMRNILNGSVQKPHAVTFVNDHNSQPGALSEF 374
 DB 329 YNOSVDFVPLHYNLVNASNGYFDMRNILNGSVQKPHAVTFVNDHNSQPGALSEF 388
 QY 375 VQSMFKPLAYALLITREQGYSVFYGDYGI---PTHGVSMSKIDPLQARQYAYGT 431
 DB 389 VQSMFKPLAYALLITREQGYSVFYGDYGI---PTHGVSMSKIDPLQARQYAYGT 448
 QY 432 QHDFPHDHLITGTRBDSHPNSGLATIMSDFGCKMXYVYKAKAGVWRITGNRSG 491
 DB 449 QHDFPHDHLITGTRBDSHPNSGLATIMSDFGCKMXYVYKAKAGVWRITGNRSG 508
 QY 492 TVTINADGMGNFTVNGAVSWWVK 516
 DB 509 TVTINADGMGNFTVNGAVSWWVK 533

RESULT 6

ID 081YJ4 PRELIMINARY; PRT; 513 AA.
 AC 081YJ4; 06HYU0; 06K003; 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE Alpha-amy1ase.
 GN Name:amy1; Ordered:locusNames=BA5351, BAS3291, GBA33551;
 OS Bacillus anthracis.
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 OX NCBI_TaxID=1392;
 RP SEQUENCE FROM N.A.
 RC STRAIN=Ames / isolate Porton;
 RX MEDLINE=22608414; PubMed=12721629; DOI=10.1038/nature01586;
 RA Read T.D., Peterson S.N., Tourasse N.J., Baillye L.W., Paulsen I.T.,
 RA Nelson K.E., Tettelin H., Fouts D.E., Eisen J.A., Gill S.R.,

RA Holtzaple E.K., Okstad O.A., Helgason E., Rilstone J., Wu M.,
 RA Kolonay J.F., Beanan M.J., Dodson R.J., Brinkac L.M., Gwinn M.L.,
 RA DeBoy R.T., Madpu R., Daugherty S.C., Dukin A.S., Haft D.H.,
 RA Nelson M.C., Peterson J.D., Pop M., Kouri H.M., Redune D.,
 RA Benton J.L., Mahmoud Y., Jiang L., Hance I.R., Weidman J.F.,
 RA Berry K.J., Platt R.D., Wolf A.M., Watkins K.L., Nierman W.C.,
 RA Hazen A., Cline R.T., Redmond C., Thwaitte J.E., White O.,
 RA Salzberg S.L., Thomson B., Friedlander A.M., Koehler T.M.,
 RA Hanna P.C., Koistee A.-B., Fraser C.M.;
 RA "The genome sequence of Bacillus anthracis Ames and comparison to
 RT closely related bacteria.";
 RL Nature 423:81-86(2003).
 RN [2]

RP SEQUENCE FROM N.A.
 RC STRAIN=Ames / isolate 0581;
 RA Ravel J., Rasko D.A., Shumway M.F., Jiang L., Cer R.Z., Federova N.B.,
 RA Wilson M., Stanley S., Decker S., Read T.D., Salzberg S.L.,
 RA Fraser C.M.;
 RL "Bacillus anthracis comparative genomics.";
 RN Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
 RN [3]

RP SEQUENCE FROM N.A.
 RC STRAIN=Stearne,
 RA Bretlin T.S., Bruce D., Challacombe J.F., Gilna P., Han C., Hill K.,
 RA Hitchcock P., Jackson P., Keim P., Longmire J., Lucas S., Okinaka R.,
 RA Richardson P., Rubin E., Tice H.;
 RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB017035; AAP27311.1; -;
 DR EMBL; AB017334; AAP28659.1; -;
 DR EMBL; AB017225; AAP25599.1; -;
 DR HSSP; P06278; 1VJ5.
 DR TIGR; BA3551; -;
 DR TIGR; GRAA3551; -;
 DR GO; GO:0004556; F:alpha-amyase activity; IEA.
 DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
 DR InterPro; IPR006047; Alpha_amy1_cat.
 DR InterPro; IPR006589; Alp_amy1_cat_sub.
 DR Pfam; PF00128; Alpha-amy1ase; 1.
 DR SMART; SM00642; Amy; 1.
 KW Complete proteome.
 SQ SEQUENCE 513 AA; 58445 MW; 558D6EF282FD159B CRC64;

Query Match 68.2%; Score 1952.5; DB 2; Length 513;
 Best Local Similarity 67.1%; Pred. No. 1.6e-123;
 Matches 339; Conservative 72; Mismatches 89; Indels 5; Gaps 3;

QY 16 LAVAVLFPYMTPEPAQAHNG-TNGTMMQYFEMHLPNDGNHNRRLRDAANLKSQGITAVW 74
 DB 10 LSVVMEFLPSIYGSKAYADTVNNGTLMQYFEWYAPNDGNHNRRLRDAENLQKIGITSW 69
 QY 75 IPPAMKTSQNDVGYGAYDLIDLGEFNQKGTVRTKGTSGQLQCAVTSLKNGIQYVGV 134
 DB 90 IPPAYKGTQNDVGYGAYDLIDLGEFNQKGTVRTKGTSGQLQCAVTSLKNGIQYVGV 129
 QY 135 VNMHKGADGTEWNAVEVNRNSNRNOISGEYTIEMTKEDPFGRGNTSHFKRWYHPD 194
 DB 130 VNMHKGADGTEWNAVEVNRNSNRNOISGEYTIEMTKEDPFGRGNTSHFKRWYHPD 189
 QY 195 GTDMDSROLQNKIKYFRGTGKAMDEVDLENGNYDLYADIDMDHPEVINELRWGW 254
 DB 190 GTDMDSROLQNKIKYFRGTGKAMDEVDLENGNYDLYADIDMDHPEVINELRWGW 248
 QY 255 YNTNLMDGFRIDAVYKIKSYTRDMLTHVRNTTGPMPFAVAFWKNDLAIENYLNKTS 314
 DB 249 YANELMDGFRIDAVYKIKSYTRDMLTHVRNTTGPMPFAVAFWKNDLAIENYLNKTS 308
 QY 315 MNHSVDFVPLHYNLVNASNGYFDMRNILNGSVQKPHAVTFVNDHNSQPGALSEF 374
 DB 309 YNOSVDFVPLHYNLVNASNGYFDMRNILNGSVQKPHAVTFVNDHNSQPGALSEF 368
 QY 375 VQSMFKPLAYALLITREQGYSVFYGDYGI---PTHGVSMSKIDPLQARQYAYGT 431
 DB 369 VQSMFKPLAYALLITREQGYSVFYGDYGI---PTHGVSMSKIDPLQARQYAYGT 428

Qy 432 QHDYFDHDDIGWTRREGDSHPNSGLATIMSDPGSGKMMYVGGKAKQVWRDITGNSG 491
 Db 429 QRDYLDHDDVIGWTRREGDSVHANSGLATLISDGPSSKMMYVGGKAKQVWRDITGNTN 488
 Qy 492 TTTINADGKGNFTVNGAVSVWVKQ 516
 Db 489 TTTINKDGMGQFHVSGGSVSIVVQ 513

RESULT 7

Q6HFU3 PRELIMINARY; PRT; 513 AA.
 ID Q6HFU3
 AC Q6HFU3;
 DT 05-JUL-2004 (TREMBlrel. 27, Created)
 DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
 DE Alpha-amylase (1,4-alpha-D-glucan glucanohydrolase) (EC 3.2.1.1).
 GN Name=amyS; OrderedLocustName=BT9727_3261;
 OS Bacillus thuringiensis (subsp. konkukian).
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 CX NCBI_TaxID=180856;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=97-27;
 RA Bretin T.S., Bruce D., Challacombe J.F., Gilna P., Han C., Hill K.,
 RA Hitchcock P., Jackson P., Keim P., Longmire J., Lucas S., Okinaka R.,
 RA Richardson P., Rubin E., Rice H.;
 RL "Complete genome sequence of Bacillus thuringiensis 97-27.";
 RL Submitted (JUN-2004) to the EMBL/Genbank/DBJ databases.
 DR EMBL; AE017355; AAT60457.1;
 DR GO; GO:0004556; F:alpha-amylase activity; IEA.
 DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
 DR InterPro; IPR006047; Alpha_amyl_cat.
 DR InterPro; IPR006589; Alp_amyl_cat_sub.
 DR Pfam; PF00128; Alpha-amylase; 1.
 DR SMART; SM00642; Amy; 1.
 DR Complete proteome.
 SK SEQUENCE 513 AA; 58342 MW; CA9683F6C31A26C3 CRC64;

Query Match 68.1%; Score 1948.5; DB 2; Length 513;
 Best Local Similarity 66.9%; Pred. No. 2.9e-123;
 Matches 338; Conservative 73; Mismatches 89; Indels 5; Gaps 3;
 Qy 16 LAVAVLPEPTPEPAQAHNG--TNGTMMQYFEMHLNDNNHNRRLRDPDANKSGITVAV 74
 Db 10 LSVVLPSPISYGSKVAVDTINNGTLMQYFEMVAPSDNGNHRRLRTDAENLAKGITSVW 69
 Qy 75 IPPAMKGTQNDVGVAVDYLDELGNQKGTVRTYGRSLOQAVTSLKNNGIQVYGDV 134
 Db 70 IPPAYKGTQNDVGVAVDYLDELGNQKGTVRTYGRSLOQAVTSLKNNGIQVYGDV 129
 Qy 135 VMAHKGADGTEVNAVEVNSNRNOEISGEYTI EAMTKFDFPGKNTSHFKRWYFD 194
 Db 130 VMAHKGADGTEVNAVEVNSNRNOEISGEYTI EAMTKFDFPGKNTSHFKRWYFD 189
 Qy 195 GTMDQSORLONKTYKPGCTKAMDWEVDINGVYDYTMVADIMDHEVINEILRNQVW 254
 Db 190 GTMDQSORLONKTYKPGCTKAMDWEVDINGVYDYTMVADIMDHEVINEILRNQVW 248
 Qy 255 YTNLTNLDFGFIADVAVKIKYSTRDMLTVANTTGKPFVAAEPKNDLAIENYLVNTS 314
 Db 249 YANLNLDFGFIADVAVKIKYSTRDMLTVANTTGKPFVAAEPKNDLAIENYLVNTS 308
 Qy 315 WNSHVFDPVPLHYNLVNASNGSGYFDMRNILNGSVVQKPIHAVTFVDNHSQPEALSEF 374
 Db 309 YNSGVFDPVPLHYNLVNASNGSGYFDMRNILNGSVVQKPIHAVTFVDNHSQPEALSEF 368
 Qy 375 VQSMFKPLAVYLLITREGYSVRYGDTYGI---PTHGVPMKSKIDPLQARQTYAVGT 431
 Db 369 VSAFMKPLAVYLLITREGYSVRYGDTYGI---PTHGVPMKSKIDPLQARQTYAVGT 428
 Qy 432 QHDYFDHDDIGWTRREGDSHPNSGLATIMSDPGSGKMMYVGGKAKQVWRDITGNSG 491

Db 429 QRDYLDHDDVIGWTRREGDSVHANSGLATLISDGPSSKMMYVGGKAKQVWRDITGNTN 488
 Qy 492 TTTINADGKGNFTVNGAVSVWVKQ 516
 Db 489 TTTINKDGMGQFHVSGGSVSIVVQ 513

RESULT 8

AMY_BACLI STANDARD; PRT; 512 AA.
 ID AMY_BACLI
 AC P06278; Q94171;
 DT 01-JAN-1988 (Rel. 06, Created)
 DT 01-JAN-1988 (Rel. 06, Last sequence update)
 DE Alpha-amylase precursor (EC 3.2.1.1) (1,4-alpha-D-glucan glucanohydrolase) (BLA).
 GN Name=amyS; Synonyms=amyL;
 OS Bacillus licheniformis.
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 CX NCBI_TaxID=1402;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 27811;
 RA MEDLINE=86111694; PubMed=2418011;
 RA Yuuki T., Nomura T., Tezuka H., Tsuboi A., Yamagata H., Tsukagoshi N.,
 RA Udaoka S.;
 RL "Complete nucleotide sequence of a gene coding for heat- and pH-stable
 RL alpha-amylase of Bacillus licheniformis: comparison of the amino acid
 RL sequences of three bacterial liquefying alpha-amylases deduced from
 RL the DNA sequences.";
 RL J. Biochem. 98:1147-1156(1985).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=86195857; PubMed=3009417;
 RA Gray G.L., Mainzer S.E., Rey M.W., Lamsa M.H., Kindle K.L.,
 RA Carmona C., Reunadt C.;
 RL "Structural genes encoding the thermostable alpha-amylase of Bacillus
 RL stearotheophilus and Bacillus licheniformis.";
 RL J. Bacteriol. 166:635-643(1986).
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Shalhoub M., Ziaei A.A., Ghaemi N., Pourbabaee A.A.;
 RL "An unusual DNA sequence encoded a hyperthermostable alpha-amylase.";
 RL Submitted (OCT-2001) to the EMBL/Genbank/DBJ databases.
 RN [4]
 RP SEQUENCE OF 1-104 FROM N.A.
 RX MEDLINE=84185455; PubMed=6609154;
 RA Stephens M.A., Ortlepp S.A., Ollington J.F., McConnell D.J.;
 RL "Nucleotide sequence of the 5' region of the Bacillus licheniformis
 RL alpha-amylase gene: comparison with the B. amyloliquefaciens gene.";
 RL J. Bacteriol. 158:369-372(1984).
 RN [5]
 RP SEQUENCE OF 1-29 FROM N.A.
 RX MEDLINE=89213924; PubMed=2540150;
 RA Loeide B.M., Chambliss G.H., McConnell D.J.;
 RL "Bacillus licheniformis alpha-amylase gene, amyL, is subject to
 RL promoter-independent catapolytic repression in Bacillus subtilis.";
 RL J. Bacteriol. 171:2435-2442(1989).
 RN [6]
 RP SEQUENCE OF 30-47.
 RX MEDLINE=92098050; PubMed=6172419;
 RA Kuhn H., Pletzek P.P., Lampen J.O.;
 RL "N-terminal amino acid sequence of Bacillus licheniformis alpha-
 RL amylase: comparison with Bacillus amyloliquefaciens and Bacillus
 RL subtilis enzymes.";
 RL J. Bacteriol. 149:372-373(1982).
 RN [7]
 RP MAPPING OF SUBSTRATE-BINDING SITE.
 RX MEDLINE=21992788; PubMed=11997021; DOI=10.1016/S0014-5793(02)02649-2;
 RA Kandra L., Gyemant G., Remenyik J., Hovanszki G., Liptak A.;
 RL "Action pattern and substrate mapping of Bacillus licheniformis alpha-
 RL amylase (Bla) with modified maltotriogalactosaccharide substrates.";

FEBS Lett. 518:79-82(2002).

[8] RT MUTAGENESIS OF HIS-64; HIS-162; HIS-276; HIS-322; HIS-435 AND HIS-479.
 RC STRAIN=ATCC 6598;
 RX MEDLINE=22538505; PubMed=12540849; DOI=10.1074/jbc.M212618200;
 RA Machius M., Declerck N., Huber R., Wiegand G.,
 RT "Kinetic stabilization of Bacillus licheniformis alpha-amylase through
 RL introduction of hydrophobic residues at the surface."
 J. Biol. Chem. 278:11546-11553(2003).

[9] RT "Use of amber suppressors to investigate the thermostability of
 RT Bacillus licheniformis alpha-amylase. Amino acid replacements at 6
 RT histidine residues reveal a critical position at His-133."
 J. Biol. Chem. 265:15481-15488(1990).

[10] RT MUTAGENESIS OF ALA-238.
 RC STRAIN=ATCC 6598;
 RX MEDLINE=96367070; PubMed=8771184;
 RA Declerck N., Joyet P., Trosset J.Y., Garnier J., Galliard C.,
 RT "Hyperthermostable mutants of Bacillus licheniformis alpha-amylase:
 RT multiple amino acid replacements and molecular modelling."
 Protein Eng. 8:1029-1037(1995).

[11] RT MUTAGENESIS OF ASP-150; ASN-155; ARG-175; ASP-193; ASN-201; GLN-207;
 RC ASN-217; ASN-219; ASN-221; ASP-229; ASP-233; ALA-298; GLU-300; GLN-359
 AND GLU-365.
 RX STRAIN=ATCC 6598;
 RX MEDLINE=20425100; PubMed=10966804; DOI=10.1006/jmbi.2000.4025;
 RA Declerck N., Machius M., Wiegand G., Huber R., Galliard C.,
 RT "Probing structural determinants specifying high thermostability in
 RT Bacillus licheniformis alpha-amylase."
 J. Mol. Biol. 301:1041-1057(2000).

[12] RT MUTAGENESIS OF GLN-293 AND ASN-294.
 RC MEDLINE=ATCC 6598;
 RX MEDLINE=22622182; PubMed=12736372; DOI=10.1093/proeng/gzg032;
 RA Declerck N., Machius M., Joyet P., Wiegand G., Huber R.,
 RT "Hyperthermostabilization of Bacillus licheniformis alpha-amylase and
 RT modulation of its stability over a 50 degrees C temperature range."
 Protein Eng. 16:287-293(2003).

[13] RT MUTAGENESIS OF TRP-292 AND VAL-315.
 RC STRAIN=ATCC 27811;
 RX MEDLINE=22797417; PubMed=12915728; DOI=10.1093/protein/gzg060;
 RA Rivera M.H., Lopez-Munguia A., Soberon X., Saab-Rincon G.,
 RT "Alpha-amylase from Bacillus licheniformis mutants near to the
 RT catalytic site: effects on hydrolytic and transglycosylation
 RT activity."
 Protein Eng. 16:505-514(2003).

[14] RT X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
 RC STRAIN=ATCC 27811;
 RX MEDLINE=95182462; PubMed=7877175;
 RA Machius M., Wiegand G., Huber R.,
 RT "Crystal structure of calcium-depleted Bacillus licheniformis alpha-
 RT amylase at 2.2-A resolution."
 J. Mol. Biol. 246:545-559(1995).

[15] RT X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
 RC MEDLINE=98212915; PubMed=9551551; DOI=10.1016/S0969-2126(98)00032-X;
 RA Machius M., Declerck N., Huber R., Wiegand G.,
 RT "Activation of Bacillus licheniformis alpha-amylase through a
 RT disorder-->order transition of the substrate-binding site mediated by
 RT a calcium-sodium-calcium metal triad."
 Structure 6:281-292(1998).

[16] RT X-RAY CRYSTALLOGRAPHY (1.7 ANGSTROMS) OF MUTANT
 RC MEDLINE=2034196; PubMed=10924103; DOI=10.1021/bi0000317;
 RX Brzozowski A.M., Lawton D.M., Turkemburg J.P., Bisgaard-Frantzen H.,
 RA Svendsen A., Borchert T.V., Dauter Z., Wilson K.S., Davies G.J.,
 RT "Structural analysis of a chimeric bacterial alpha-amylase. High-
 RT resolution analysis of native and ligand complexes."
 Biochemistry 39:9099-9107(2000).

[17] RT X-RAY CRYSTALLOGRAPHY (1.7 ANGSTROMS) OF MUTANT
 RC H162V/N219F/A238V/Q293S/N294Y.

RC STRAIN=ATCC 6598;
 RX MEDLINE=22538505; PubMed=12540849; DOI=10.1074/jbc.M212618200;
 RA Machius M., Declerck N., Huber R., Wiegand G.,
 RT "Kinetic stabilization of Bacillus licheniformis alpha-amylase through
 RL introduction of hydrophobic residues at the surface."
 J. Biol. Chem. 278:11546-11553(2003).

[1] RT "Use of amber suppressors to investigate the thermostability of
 RT Bacillus licheniformis alpha-amylase. Amino acid replacements at 6
 RT histidine residues reveal a critical position at His-133."
 J. Biol. Chem. 265:15481-15488(1990).

[2] RT MUTAGENESIS OF ALA-238.
 RC STRAIN=ATCC 6598;
 RX MEDLINE=96367070; PubMed=8771184;
 RA Declerck N., Joyet P., Trosset J.Y., Garnier J., Galliard C.,
 RT "Hyperthermostable mutants of Bacillus licheniformis alpha-amylase:
 RT multiple amino acid replacements and molecular modelling."
 Protein Eng. 8:1029-1037(1995).

[3] RT MUTAGENESIS OF ASP-150; ASN-155; ARG-175; ASP-193; ASN-201; GLN-207;
 RC ASN-217; ASN-219; ASN-221; ASP-229; ASP-233; ALA-298; GLU-300; GLN-359
 AND GLU-365.
 RX STRAIN=ATCC 6598;
 RX MEDLINE=20425100; PubMed=10966804; DOI=10.1006/jmbi.2000.4025;
 RA Declerck N., Machius M., Wiegand G., Huber R., Galliard C.,
 RT "Probing structural determinants specifying high thermostability in
 RT Bacillus licheniformis alpha-amylase."
 J. Mol. Biol. 301:1041-1057(2000).

[4] RT MUTAGENESIS OF GLN-293 AND ASN-294.
 RC MEDLINE=ATCC 6598;
 RX MEDLINE=22622182; PubMed=12736372; DOI=10.1093/proeng/gzg032;
 RA Declerck N., Machius M., Joyet P., Wiegand G., Huber R.,
 RT "Hyperthermostabilization of Bacillus licheniformis alpha-amylase and
 RT modulation of its stability over a 50 degrees C temperature range."
 Protein Eng. 16:287-293(2003).

[5] RT MUTAGENESIS OF TRP-292 AND VAL-315.
 RC STRAIN=ATCC 27811;
 RX MEDLINE=22797417; PubMed=12915728; DOI=10.1093/protein/gzg060;
 RA Rivera M.H., Lopez-Munguia A., Soberon X., Saab-Rincon G.,
 RT "Alpha-amylase from Bacillus licheniformis mutants near to the
 RT catalytic site: effects on hydrolytic and transglycosylation
 RT activity."
 Protein Eng. 16:505-514(2003).

[6] RT X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
 RC STRAIN=ATCC 27811;
 RX MEDLINE=95182462; PubMed=7877175;
 RA Machius M., Wiegand G., Huber R.,
 RT "Crystal structure of calcium-depleted Bacillus licheniformis alpha-
 RT amylase at 2.2-A resolution."
 J. Mol. Biol. 246:545-559(1995).

[7] RT X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
 RC MEDLINE=98212915; PubMed=9551551; DOI=10.1016/S0969-2126(98)00032-X;
 RA Machius M., Declerck N., Huber R., Wiegand G.,
 RT "Activation of Bacillus licheniformis alpha-amylase through a
 RT disorder-->order transition of the substrate-binding site mediated by
 RT a calcium-sodium-calcium metal triad."
 Structure 6:281-292(1998).

[8] RT X-RAY CRYSTALLOGRAPHY (1.7 ANGSTROMS) OF MUTANT
 RC MEDLINE=2034196; PubMed=10924103; DOI=10.1021/bi0000317;
 RX Brzozowski A.M., Lawton D.M., Turkemburg J.P., Bisgaard-Frantzen H.,
 RA Svendsen A., Borchert T.V., Dauter Z., Wilson K.S., Davies G.J.,
 RT "Structural analysis of a chimeric bacterial alpha-amylase. High-
 RT resolution analysis of native and ligand complexes."
 Biochemistry 39:9099-9107(2000).

[9] RT X-RAY CRYSTALLOGRAPHY (1.7 ANGSTROMS) OF MUTANT
 RC H162V/N219F/A238V/Q293S/N294Y.

EMBL: X03236; CAA26981.1; -
 EMBL: M38570; AAA22226.1; -
 EMBL: M13256; AAA22240.1; -
 EMBL: K01984; AAA22193.1; -
 EMBL: AF438149; AAO26743.1; -
 EMBL: M26412; AAA22237.1; -
 EMBL: A17930; CAA01355.1; -
 PIR: A91997; ALBSL.
 PDB: 1BPL; X-ray; A=30-512.
 PDB: 1BPL; X-ray; A=30-218, B=219-512.
 PDB: 1E3X; X-ray; A=-.
 PDB: 1E3X; X-ray; A=-.
 PDB: 1E40; X-ray; A=-.
 PDB: 1E43; X-ray; A=-.
 PDB: 1O80; X-ray; A=30-512.
 PDB: 1VUS; X-ray; A=30-512.
 InterPro: IPR006047; Alpha_amy1_cat.
 InterPro: IPR006046; Glyco_hydro_13.
 Pfam: PF00128; Alpha-amylase_1.
 PRINTS: PR00110; ALPHAMYLASE.
 KX 3D-structure; Calcium-binding; Carbohydrate metabolism;
 KW Direct protein sequencing; Glycosidase; Hydrolyase; Signal.
 FT CHAIN 1 29
 FT ACT SITE 30 512 Alpha-amylase.
 FT ACT SITE 260 260 Nucleophile.
 FT ACT SITE 290 290 Proton donor.
 FT ACT SITE 357 357 By similarity.
 FT METAL 133 133 Calcium 1.
 FT METAL 190 190 Calcium 2 and sodium.
 FT METAL 210 210 Calcium 2 (via carboxyl oxygen).
 FT METAL 212 212 Calcium 2 and sodium.
 FT METAL 223 223 Calcium 1 and sodium.
 FT METAL 229 229 Calcium 1 and sodium.
 FT METAL 231 231 Calcium 2.
 FT METAL 233 233 Calcium 2.
 FT METAL 264 264 Calcium 1 (via carbonyl oxygen).
 FT METAL 329 329 Calcium 3 (via carboxyl oxygen).

Query Match 67.9%; Score 1942; DB 1; Length 512;
 Best Local Similarity 66.6%; Pred. No. 8e-123;
 Matches 347; Conservative 71; Mismatches 89; Indels 14; Gaps 5;

QY 1 MKLHNRILISVLITLLAVAVLPFYMTPEPAQAHNGTNGTMOYFEWHLRNDGHNMRIRD 60
 DB 1 MKQQRKLYARLLTLTLFALIFLLPHSAAAA---NLNGTLMQYFEWMPNDGQHWKRLQW 56

Qy 61 DAANLKSQGTAAWIIPAMKGTSONDVGYGAYDYLDEGFNOKGTVRTKYRGSOLQAV 120
 Db 57 DSAFLAHEGITAAMIIPAYKGTSDADVGAYDYLDEGFNOKGTVRTKYRGSOLQAV 116
 Qy 121 TSLKNGIOVYGDVVMNHKGGADGTEMVNAVEVNRNSNNOEISEGYTTEAWTKDFPGRG 180
 Db 117 KSLSRDINIVYGDVVMNHKGGADGTEMVNAVEVNRNSNNOEISEGYTTEAWTKDFPGRG 176
 Qy 181 NTHSNFKRWYHFGTMDGSRQONKIYKRGTKAMDEVDIENGNYDYLMTADIDMD 240
 Db 177 STYSDPFKWHYHFGTMDGSRQONKIYKRGTKAMDEVDIENGNYDYLMTADIDMD 233
 Qy 241 HPEYINELRWGVYVYTLNLNDGFRIDAVKHIKSYTRDMULTYRNTTKGMPFAVAEPFK 300
 Db 234 HPDVAIEIKRWGTYANELQDGFRLDAVKIKSFLDMVNHVREKTKGMPFAVAETWQ 293
 Qy 301 NDLAIEYINLKTSMNSVDFVPLHYNLVNASNGYFDMKNIINGSVYQKPIHAATFV 360
 Db 294 NDLAGLENYLKTSMNSVDFVPLHYQFHAASGQGGYDMKLNSTVSKHPLKAVTFV 353
 Qy 361 DNHSQGEALLESVQSWFKPLAYALLITREOGTSPVYGYGIPTHG-----VPSMKS 415
 Db 354 DNHDTPQGSLESTVQTFKPLAYALLITRESGPVQVFGDMYG--TKGDSOREIPLAKH 411
 Qy 416 KIDPLQARQTYAGTGHDFDHHDIIGWTRGDSHPNSGLATIMSPDPCGNKMMVYVK 475
 Db 412 KIEPIKARKOYAGAGHDYFDHHDIVGWTREGSSVANSGLAALITDGPAGAKMYGK 471
 Qy 476 HKAGQVRDITGNRSQVTTINADGMNFTVNGAVSVWVQ 516
 Db 472 QNAGETWHDITGNRSEPVINSBGMEFHVNGSVSIYVOR 512

RESULT 9

Q65MX0 PRELIMINARY; PRT; 512 AA.
 AC Q65MX0; TREMBLrel. 28. Created)
 DT 25-OCT-2004 (TREMBLrel. 28. Last sequence update)
 DT 25-OCT-2004 (TREMBLrel. 28. Last annotation update)
 DE Alpha-amylose (BC 3.2.1.1) (Trehalose-6-phosphate hydrolase).
 GN ORFNames=BL00499, BL100656;
 OS Bacillus licheniformis DSM 13.
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 OX NCBI_TaxID=279010;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=DSM 13;
 RX PubMed=15383718;
 RA Veith B., Herzberg C., Steckel S., Feesche J., Maurer K.H.,
 RA Ehrenreich P., Baumeier S., Henne A., Liesegang H., Merkl R.,
 RA Ehrenreich A., Gottschalk G.;
 RT "The Complete Genome Sequence of Bacillus licheniformis DSM13, an
 RT Organism with Great Industrial Potential.";
 RL J. Mol. Microbiol. Biotechnol. 7:204-211 (2004).
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 14580;
 RA Ray M.W., Ramaiya P., Nelson B.A., Brody-Karpin S.D., Zaretsky E.J.,
 RA Tang M., de Leon A.L., Xiang H., Guest V., Clausen I.G., Olsen P.B.,
 RA Rasmussen M.D., Andersen J.T., Jorgensen P.L., Larsen T.S.,
 RA Sorokin A., Bolotin A., Lapidus A., Galleron N., Ehrlich S.D.,
 RA Berka R.M.;
 RT "Complete genome sequence of the industrial bacterium Bacillus
 RT licheniformis and comparisons with closely related Bacillus species.";
 RL Genome Biol. 5:R77-R77(2004).
 DR EMBL; AE017333; AAU39594.1; -
 DR EMBL; CP000002; AAU2245.1; -
 KW Glycosidase; Hydrolase
 SQ SEQUENCE 512 AA; 58529 MW; E3F8F560C3419D9D CRC64;

Query Match 67.6%; Score 1936; DB 2; Length 512;
 Best Local Similarity 66.4%; Pred. No. 2e-122;

Matches 346; Conservative 71; Mismatches 90; Indels 14; Gaps 5;
 Qy 1 MKNLRILSVTLTLLAVAVLPYMTPEPAQHNGTGMQVEMFLPNDGNMNLRD 60
 Db 1 MKQQRUYARLLPLFLFLIPHSAAAA---NLKGLMQVEMWPNPGQMKRLQN 56
 Qy 61 DAANLKSQGTAAWIIPAMKGTSONDVGYGAYDYLDEGFNOKGTVRTKYRGSOLQAV 120
 Db 57 DSAFLAHEGITAAMIIPAYKGTSDADVGAYDYLDEGFNOKGTVRTKYRGSOLQAV 116
 Qy 121 TSLKNGIOVYGDVVMNHKGGADGTEMVNAVEVNRNSNNOEISEGYTTEAWTKDFPGRG 180
 Db 117 KSLSRDINIVYGDVVMNHKGGADGTEMVNAVEVNRNSNNOEISEGYTTEAWTKDFPGRG 176
 Qy 181 NTHSNFKRWYHFGTMDGSRQONKIYKRGTKAMDEVDIENGNYDYLMTADIDMD 240
 Db 177 STYSDPFKWHYHFGTMDGSRQONKIYKRGTKAMDEVDIENGNYDYLMTADIDMD 233
 Qy 241 HPEYINELRWGVYVYTLNLNDGFRIDAVKHIKSYTRDMULTYRNTTKGMPFAVAEPFK 300
 Db 234 HPDVAIEIKRWGTYANELQDGFRLDAVKIKSFLDMVNHVREKTKGMPFAVAETWQ 293
 Qy 301 NDLAIEYINLKTSMNSVDFVPLHYNLVNASNGYFDMKNIINGSVYQKPIHAATFV 360
 Db 294 NDLAGLENYLKTSMNSVDFVPLHYQFHAASGQGGYDMKLNSTVSKHPLKAVTFV 353
 Qy 361 DNHSQGEALLESVQSWFKPLAYALLITREOGTSPVYGYGIPTHG-----VPSMKS 415
 Db 354 DNHDTPQGSLESTVQTFKPLAYALLITRESGPVQVFGDMYG--TKGDSOREIPLAKH 411
 Qy 416 KIDPLQARQTYAGTGHDFDHHDIIGWTRGDSHPNSGLATIMSPDPCGNKMMVYVK 475
 Db 412 KIEPIKARKOYAGAGHDYFDHHDIVGWTREGSSVANSGLAALITDGPAGAKMYGK 471
 Qy 476 HKAGQVRDITGNRSQVTTINADGMNFTVNGAVSVWVQ 516
 Db 472 QNAGETWHDITGNRSEPVINSBGMEFHVNGSVSIYVOR 512

RESULT 10

Q9RQ78 PRELIMINARY; PRT; 519 AA.
 AC Q9RQ78; TREMBLrel. 13. Created)
 DT 01-MAY-2000 (TREMBLrel. 13. Last sequence update)
 DT 01-JUN-2003 (TREMBLrel. 24. Last annotation update)
 DE Raw starch digesting amylase precursor.
 OS Cytophaga sp.
 OC Bacteria; Bacteroidetes; Sphingobacteriales;
 OC Flexibacteraceae; Cytophaga.
 OX NCBI_TaxID=29535;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=22083510; PubMed=12089056;
 RX DOI=10.1128/AEM.68.7.3651-3654.2002;
 RA Jeang C.L., Chen L.S., Chen W.Y., Shiau R.J.;
 RT "Cloning of a gene encoding raw-starch-digesting amylase from a
 RT Cytophaga sp. and its expression in Escherichia coli.";
 RL Appl. Environ. Microbiol. 68:3651-3654(2002).
 CC -1- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.
 DR EMBL; AF067653; AF00567.1; -
 DR HSSP; P00692; IE43.
 DR GO; GO:0004556; F:alpha-amylase activity; IEA.
 DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
 DR InterPro; IPR006047; Alpha_amyl_cat.
 DR InterPro; IPR006589; Alp_amyl_cat_sub.
 DR InterPro; IPR006046; Glyco_hydro_13.
 DR Pfam; PF00128; Alpha-amylase; 1.
 DR PRINTS; PR00110; ALPHAMYLASE.
 DR SMART; SM00642; Amy; 1.
 KW Signal.
 FT SIGNAL 1 57 Potential.
 FT CHAIN 58 519 raw starch digesting amylase.

SQ SEQUENCE 519 AA; 56337 MW; 3E6B8A4DF98B163 CRC64;
 Query Match 67.2%; Score 1923.5; DB 2; Length 519;
 Best Local Similarity 66.4%; Pred. No. 1.4e-121;
 Matches 340; Conservative 70; Mismatches 93; Indels 9; Gaps 3;

QY 8 ISVLLTLLAAVAVLPYMTPEPAQAHNNGTGMQYFEMHLPDGNHNRRLDDAANKS 67
 Db 14 ITMFSTLLV-----PSIAQPKAKAAATLGTMMQYFEMWVPNDGOQWRLRLTDAAYLS 68
 QY 68 KGLTAWIPRPMKGTSONDVGYGAYDYLDELGEFNQKGYRTKYGTSRLOGAATSKKNG 127
 Db 69 VGTAAVTPPAYKGTSDADVGYDYDYLDELGEFNQKGYRTKYGTSRLOGAATSKKNG 128
 QY 128 IQYGVGVVNMHKGADGTEMNNAVEVNRNNOEISGEYTIEMTKRDPFGKNTSHFK 187
 Db 129 IQYGVGVVNMHKGADGTEMNNAVEVNRNNOEISGEYTIEMTKRDPFGKNTSHFK 188
 QY 188 WRVYHEDGTWDSROLQNKIKYFRGTGKAMDEVDIENGNYTLMYADIDMDHPEVINE 247
 Db 189 WQMFHFGDTWDSRSL-SRIKFRGTGKAMDEVSSENGNYDLYMAYADIDYDHPVINE 247
 QY 248 LRMMGVYNTLTMLDGFRIADVAKIKSYTRDWLTHVNTTGGKPMFAVAFMKDLAIE 307
 Db 248 MKKMGVYNAEVLGDRIDAVKIKSYFLKDWVDAARATKEMFTVGEYMGNDLGALN 307
 QY 308 NYLKTSMNHSVDPDLPHYNLNYNNSGGYFDMENILNGSVQKPIHATPVNDHDSQ 367
 Db 308 NYLAKVNYNOSLPDAPLHYNFYASTGGYDYDMENILNNTLVASNPKATLVLENHDTOP 367
 QY 368 GEALIESVQSWFKRLAVALITREOGYPSVFGYGY---GLPHYGSMSKSIDPLLOAR 424
 Db 368 GQSLSTSVQWPKFLAVALITREOGYPSVFGYGYGYTTREIPALSKIEPLKAR 427
 QY 425 QTYAVGTQHDYFDHDIIGTREGSSHPNSGLATINSDGPGKXMMYVQKRAQGVWRD 484
 Db 428 KDYAVGTQHDYFDHDIIGTREGSSHPNSGLATINSDGPGKXMMYVQKRAQGVWRD 487
 QY 485 ITGNRSQVITINADGKGNFTVNGAVSVWYQ 516
 Db 488 LTGNRTDKITIGSDGYATFPVNGSVSVWYQ 519

RESULT 11
 P71034 PRELIMINARY; PRT; 521 AA.
 AC P71034; PRELIMINARY; PRT; 521 AA.
 DT 01-FEB-1997 (TREMBLrel. 02, Created)
 DT 01-FEB-1997 (TREMBLrel. 02, Last sequence update)
 DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
 DE Alpha-amylose precursor.
 OS Bacillus sp. MK 716.
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 OX NCBI_TaxID=54116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MK 716;
 RA Sidhu G.S., Chakarbarti T.,
 RL Submitted (OCT-1996) to the EMBL/Genbank/DBJ databases.
 CC -1- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.
 DR EMBL; U75445; AAB18785.1; -
 DR HSPB; P06279; IHVX.
 DR GO; GO:0004556; F:alpha-amylose activity; IEA.
 DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
 DR InterPro; IPR006047; Alpha_amy1_cat.
 DR InterPro; IPR006589; Alp_amy1_cat_sub.
 DR InterPro; IPR006046; Glyco_hydro_13.
 DR Pfam; PF00128; Alpha-amylose; 1.
 DR PRINTS; PR00110; ALPHAMYLASE.
 DR SMART; PR00110; ALPHAMYLASE.
 KW Signal.
 FT SIGNAL 1 34 Potential.
 FT CHAIN 35 521 alpha-amylose.

SQ SEQUENCE 521 AA; 59311 MW; 5612A8596D922E1 CRC64;
 Query Match 66.9%; Score 1915.5; DB 2; Length 521;
 Best Local Similarity 65.8%; Pred. No. 5e-121;
 Matches 340; Conservative 74; Mismatches 98; Indels 5; Gaps 3;

QY 1 MGLHNRITIS---VLTLLAAVAVLPYMTPEPAQAHNNGTGMQYFEMHLPDGNHNRRL 57
 Db 1 MLTFRIIRKGMFLAALRLSLFCPPGQPAKA-AAFPNGITMQYFEMWLPDQGLTWTK 59
 QY 58 LDDAANKSKGITAWEIPPMKGTSONDVGYGAYDYLDELGEFNQKGYRTKYGTSRLOG 117
 Db 60 VANEANNLSIGITLALMLPPAYKGTSDADVGYDYDYLDELGEFNQKGYRTKYGTSRLOG 119
 QY 118 GAVTSIKKNGIQYGVGVVNMHKGADGTEMNNAVEVNRNNOEISGEYTIEMTKRDPFG 177
 Db 120 QALQAHNAQMQYVADVFDHKGADGTEWDAVAVNSDRNOEISGYIQALMTKDFP 179
 QY 178 GRGNTHSNPKRMVYFDGTWDSROLQNKIKYFRGTGKAMDEVDIENGNYDLYMAYADI 237
 Db 180 GRGNTHSNPKRMVYFDGTWDSRKL-SRIKFRGTGKAMDEVDIENGNYDLYMAYADI 238
 QY 238 DMDHPEVINELRNMGVYNTLTMLDGFRIADVAKIKSYTRDWLTHVNTTGGKPMFAV 297
 Db 239 DMDHPEVINELRNMGVYNTLTMLDGFRIADVAKIKSYTRDWLTHVNTTGGKPMFAV 298
 QY 298 FKNDLAALIENTLNTSMNHSVDPDLPHYNLNYNNSGGYFDMENILNGSVQKPIHAT 357
 Db 299 YMSYDINKHANTYITKNGTMSLPDAPLHNFYASTGGYDYDMENILNNTLVASNPKAT 358
 QY 358 TFDNDHDSQPGALBSFVQSWFKPLAVALITREOGYPSVFGYGYGY---GLPHYGSMSK 417
 Db 359 TFDNDHDSQPGALBSFVQSWFKPLAVALITREOGYPSVFGYGYGYGY---GLPHYGSMSK 418
 QY 418 DPLLOARQTYAVGTQHDYFDHDIIGTREGSSHPNSGLATINSDGPGKXMMYVQKRA 477
 Db 419 DPLLOARQTYAVGTQHDYFDHDIIGTREGSSHPNSGLATINSDGPGKXMMYVQKRA 478
 QY 478 AGQVWRDITGNRSQVITINADGKGNFTVNGAVSVWYQ 514
 Db 479 AGQVWRDITGNRSQVITINADGKGNFTVNGAVSVWYQ 515

RESULT 12
 Q9KMY6 PRELIMINARY; PRT; 549 AA.
 AC Q9KMY6; PRELIMINARY; PRT; 549 AA.
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
 DE Alpha-amylose (EC 3.2.1.1).
 OS Bacillus stearothermophilus.
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Geobacillus.
 OX NCBI_TaxID=1422;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=US100;
 RA Ali M.B., Miri S., Merzghani M., Bejar S.;
 RT "Purification and sequence analysis of the atypical maltotetraose-
 forming alpha-amylose of the B. stearothermophilus US100."
 RL Enzyme Microb. Technol. 28:537-542(2001).
 CC -1- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.
 DR EMBL; Y17557; CAB93517.1; -
 DR PIR; A54541; A54541.
 DR HSPB; P06279; IHVX.
 DR GO; GO:0004556; F:alpha-amylose activity; IEA.
 DR GO; GO:0016798; F:hydrolase activity; acting on glycosyl bonds; IEA.
 DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
 DR InterPro; IPR006047; Alpha_amy1_cat.
 DR InterPro; IPR006589; Alp_amy1_cat_sub.
 DR InterPro; IPR006046; Glyco_hydro_13.
 DR Pfam; PF00128; Alpha-amylose; 1.
 DR PRINTS; PR00110; ALPHAMYLASE.

DR SMART; SM00642; Aamy; 1.
KW Glycosidase; Hydrolase.
SQ SEQUENCE 549 AA; 62582 MW; 8DA3B66DF9120BCE CRC64;

Query Match 66.9%; Score 1915.5; DB 2; Length 549;
Best Local Similarity 65.8%; Pred. No. 5.3e-121;
Matches 340; Conservative 74; Mismatches 98; Indels 5; Gaps 3;

QY 1 MCLNRIIS---VLTLLLAVALFPVMTPEAQAHNHTNGTMMQYFEMHLPNDGNHNR 57
DB 1 MLTHRIIRKGMWFLAFLLTASLFCPTGQAPKA-AAPFNGTMMQYFEMHLPDDGTL 59
QY 58 LRDDAANLKSGITAWMIPPAKMGTSQNDVGYGAYDLYDLGEFNQKGTARTKYGTSO 117
DB 60 VANANNLSSIGITATMLPPAYKGRSDVGYDLYDLGEFNQKGTARTKYGTSO 119
QY 118 GAVTSLKNGIQVYGDVVMNHKGADGTEVMNAVEVNSNNOISGEYTTBAWTKFP 177
DB 120 QAIQAAHAAGQVADVDFDHKGADGTEWDAVEVNSDRNOISGTYQIQAWTKFP 179
QY 178 GRGTHSNFKRWHPDGTMDQSOLOKNTYKPRGTGKADWEVDIENGVDYIMYADI 237
DB 180 GRGTHSNFKRWHPDGTMDQSOLOKNTYKPRGTGKADWEVDIENGVDYIMYADI 238
QY 238 DMDHPEVINELRNNGVMTNTNLNDGPRIDAVKHKYSTRDMLTHVANTTGKPFVA 297
DB 239 DMDHPEVINELRNNGVMTNTNLNDGPRIDAVKHKYSTRDMLTHVANTTGKPFVA 298
QY 298 FPKNDLAIENYLNKTSWNHVSFDPVPLHYNLVNSNSGYPDMRNILNGSVVQKPI 357
DB 299 YMSVDINLHNYITKNTGMSLFDAPLNKRYTASKSGAFDMRTMLMTNLTKQDPT 358
QY 358 TPNVNHQSOPBEALSFQSWFKPLAVALITREGYSVYGYGIPHTGVSMKSI 417
DB 359 TPNVNHQSOPBEALSFQSWFKPLAVALITREGYSVYGYGIPHTGVSMKSI 418
QY 418 DPLQARQTYAGTOHDFDHDIIIGWTRGDSHPNSGLATIMSDGSGKMMYVYGK 477
DB 419 DPLQARQTYAGTOHDFDHDIIIGWTRGDSHPNSGLATIMSDGSGKMMYVYGK 478
QY 478 AGQVARDITGNRSGTITNADGNGFTVNGAVSVW 514
DB 479 AGQVARDITGNRSGTITNADGNGFTVNGAVSVW 515

RESULT 13
ID 031193 PRELIMINARY; PRT; 549 AA.
AC 031193;
DT 01-JAN-1998 (Tremblrel. 05. Created)
DT 01-JAN-1998 (Tremblrel. 05. Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25. Last annotation update)
DE Alpha-amy-lase.
GN Name=ami;
OS Bacillus stearothermophilus.
OC Bacteria; Firmicutes; Bacilliales; Bacillaceae; Geobacillus.
OX NCBI_TaxID=1422;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 31195;
RA da Silva A.C.R., Fernandes E., Pueyo M.T.;
RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
CC -1. SIMILARITY: Belongs to family 13 of glycosyl hydrolases.
DR EMBL; AF032864; AAB86961.1; -.
DR PIR; A54541; A54541.
DR HSSP; P06279; 1HVX.
DR GO; GO:0004556; F:alpha-amy-lase activity; IEA.
DR InterPro; IPR006047; Alpha-amy-l cat.
DR InterPro; IPR006589; Alp_amy1_cat_sub.
DR InterPro; IPR006046; Glyco_hydro_13.
DR Pfam; PF00128; Alpha-amy-lase; 1.
DR PRINTS; PR00110; ALPHAMYLASE.

DR SMART; SM00642; Aamy; 1.
KW Glycosidase; Hydrolase.
SQ SEQUENCE 549 AA; 62651 MW; 2CA689EDACAD262 CRC64;

Query Match 66.9%; Score 1913.5; DB 2; Length 549;
Best Local Similarity 65.4%; Pred. No. 7.2e-121;
Matches 340; Conservative 72; Mismatches 97; Indels 11; Gaps 4;

QY 1 MCLNRIIS---VLTLLLAVALFPVMTPEAQAHNHTNGTMMQYFEMHLPNDGNH 54
DB 1 MLTHRIIRKGMWFLAFLLTASLFCPTGQAPKA-AAPFNGTMMQYFEMHLPDDGTL 56
QY 55 WNRLLDDAANLKSGITAWMIPPAKMGTSQNDVGYGAYDLYDLGEFNQKGTARTKYGTS 114
DB 57 WTKVANEANNLSSIGITATMLPPAYKGRSDVGYDLYDLGEFNQKGTARTKYGTS 116
QY 115 QLGAVTSLKNGIQVYGDVVMNHKGADGTEVMNAVEVNSNNOISGEYTTBAWTKF 174
DB 117 QYLGAVTSLKNGIQVYGDVVMNHKGADGTEWDAVEVNSDRNOISGTYQIQAWTKF 176
QY 175 DFGGTHSNFKRWHPDGTMDQSOLOKNTYKPRGTGKADWEVDIENGVDYIMYADI 234
DB 177 DFGGTHSNFKRWHPDGTMDQSOLOKNTYKPRGTGKADWEVDIENGVDYIMYADI 235
QY 235 ADIDMDHPEVINELRNNGVMTNTNLNDGPRIDAVKHKYSTRDMLTHVANTTGKPFVA 294
DB 236 ADIDMDHPEVINELRNNGVMTNTNLNDGPRIDAVKHKYSTRDMLTHVANTTGKPFVA 295
QY 295 VAEFWKNDLAIENYLNKTSWNHVSFDPVPLHYNLVNSNSGYPDMRNILNGSVVQKPI 354
DB 296 VAEFWKNDLAIENYLNKTSWNHVSFDPVPLHYNLVNSNSGYPDMRNILNGSVVQKPI 355
QY 355 HAVTFVNHQSOPBEALSFQSWFKPLAVALITREGYSVYGYGIPHTGVSMKSI 414
DB 356 HAVTFVNHQSOPBEALSFQSWFKPLAVALITREGYSVYGYGIPHTGVSMKSI 415
QY 415 SKIDPLQARQTYAGTOHDFDHDIIIGWTRGDSHPNSGLATIMSDGSGKMMYVYGK 474
DB 416 SKIDPLQARQTYAGTOHDFDHDIIIGWTRGDSHPNSGLATIMSDGSGKMMYVYGK 475
QY 475 KHKAGVARDITGNRSGTITNADGNGFTVNGAVSVW 514
DB 476 KHKAGVARDITGNRSGTITNADGNGFTVNGAVSVW 515

RESULT 14
ID AMY_BACST STANDARD; PRT; 549 AA.
AC P06279; Q45519;
DT 01-JAN-1988 (Rel. 06. Created)
DT 01-FEB-1996 (Rel. 33. Last sequence update)
DT 25-OCT-2004 (Rel. 45. Last annotation update)
DE Alpha-amy-lase precursor (EC 3.2.1.1) (1,4-alpha-D-glucan glucanohydrolase).
GN Name=amvs;
OS Bacillus stearothermophilus.
OC Bacteria; Firmicutes; Bacilliales; Bacillaceae; Geobacillus.
OX NCBI_TaxID=1422;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 35-39.
RC MEDLINE=85234394; PubMed=3924897;
RA Nakajima R., Imanaka T., Alba S.;
RT "Nucleotide sequence of the Bacillus stearothermophilus alpha-amy-lase gene."
RL J. Bacteriol. 163:401-406(1985).
RN [2]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC STRAIN=DVS/PHI300;
RA MEDLINE=86008166; PubMed=3876333;
RA Ihara H., Sasaki T., Tsuboi A., Yamagata H., Tsukagoshi N., Ueda S.;
RT "Complete nucleotide sequence of a thermophilic alpha-amy-lase gene: homology between prokaryotic and eukaryotic alpha-amy-lases at the active sites."
RL J. Biochem. 98:95-103(1985).

RN [3]
RP SEQUENCE FROM N.A.
RX STRAIN=NZ-3;
MEDLINE=86195857; PubMed=3009417;
RA Gray G.L., Mainzer S.E., Rey M.W., Lamsa M.H., Kindle K.L.,
CA Carmona C., Regnadt C.;
RT "Structural genes encoding the thermophilic alpha-amylases of *Bacillus*
ST stearothermophilus and *Bacillus licheniformis*."; *Bacteriol.* 166:635-643(1986).
RL J. Bacteriol. 166:635-643(1986).
RN [4]
RP SEQUENCE FROM N.A.
RA Suominen I., Karp M., Lautamo J., Knowles J., Mantsaeslae P.;
RT "Thermotable alpha amylase of *Bacillus stearothermophilus*: cloning,
RT expression, and secretion by *Escherichia coli*."; *J.*
RL Chaioupka J., Krumphanz V. (eds.);
RT Extracellular enzymes of microorganisms, pp.129-137, Plenum Press, New
RL York (1987).
RN [5]
RP SEQUENCE OF 1-122 FROM N.A., AND SEQUENCE OF 35-48.
RX STRAIN=DY-5;
MEDLINE=6059211; PubMed=2999073;
RA Tsukagoshi N., Iritani S., Sasaki T., Takemura T., Ihara H., Ito Y.,
CA Yamagata H., Ueda S.;
RT "Efficient synthesis and secretion of a thermophilic alpha-amylase by
RT protein-producing *Bacillus brevis* 47 carrying the *Bacillus*
ST stearothermophilus amylase gene."; *J.*
RL Bacteriol. 164:1182-1187(1985).
RN [6]
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
RX MEDLINE=21125602; PubMed=11226887;
RA Svud D., Fujimoto Z., Takase K., Matsumura M., Mizuno H.;
RT "Crystal structure of *Bacillus stearothermophilus* alpha-amylase:
RT possible factors determining the thermostability."; *J.*
RL Biochem. 123:461-468(2001).
CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic
CC linkages in oligosaccharides and polysaccharides.
CC -1- COFACTOR: Binds 3 calcium ions and 1 sodium ion per subunit.
CC -1- SUBUNIT: Monomer.
CC -1- SIMILARITY: Belongs to the glycosyl hydrolase 13 family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use by non-profit institutions as long as its content is in no way
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CC -----
CC EMBL: M11450; AAA22235.2; -;
DR EMBL: X02769; CAA26547.1; -;
DR EMBL: M57457; AAA22227.1; -;
DR EMBL: M13255; AAA22241.1; -;
DR PIR: A24436; A24436.
DR PIR: A91999; ALBSF.
DR PDB: 1HVX; X-ray; A=35-549.
DR InterPro: IPR006047; Alpha_amyl_cat.
DR InterPro: IPR006046; Glyco_hydro_13.
DR Pfam: PF00128; ALPHAAMYLASE; 1.
DR PRINTS; PR00110; ALPHAAMYLASE.
KW 3D-structure; Calcium-binding; Carbohydrate metabolism;
KW Direct protein sequencing; Glycosidase; Hydrolase; Signal.
FT STGMAL 1 34
FT CHAIN 35 549
FT ACT_SITE 268 268 Alpha-amylase.
FT ACT_SITE 298 298 Nucleophile.
FT ACT_SITE 365 365 Proton donor.
FT METAL 139 139 Calcium 1.
FT METAL 196 196 Calcium 2 and sodium.
FT METAL 218 218 Calcium 2 (via carbonyl oxygen).
FT METAL 220 220 Calcium 2 and sodium.
FT METAL 231 231 Calcium 1 and sodium.
FT METAL 237 237 Calcium 1 and sodium.
FT METAL 238 238 Sodium (via carbonyl oxygen).
FT METAL 238 238

FT METAL 239 239
FT METAL 272 272
FT METAL 337 337
FT METAL 339 339
FT METAL 440 440
FT METAL 441 441
FT METAL 444 444
FT METAL 464 464
FT CONFLICT 13 13
FT CONFLICT 19 19
FT CONFLICT 23 23
FT CONFLICT 31 31
FT CONFLICT 107 107
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FT CONFLICT 284 284
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FT CONFLICT 338 338
FT CONFLICT 342 342
FT CONFLICT 346 346
FT CONFLICT 376 376
FT CONFLICT 526 526
FT CONFLICT 527 527
FT CONFLICT 535 535
FT STRAND 42 42
FT TURN 44 44
FT TURN 48 48
FT HELIX 56 56
FT TURN 69 69
FT TURN 70 70
FT STRAND 74 74
FT STRAND 82 82
FT TURN 86 86
FT TURN 93 93
FT TURN 96 96
FT STRAND 104 104
FT TURN 105 105
FT STRAND 107 107
FT HELIX 115 115
FT TURN 128 128
FT STRAND 131 131
FT STRAND 140 140
FT STRAND 146 146
FT TURN 157 157
FT STRAND 159 159
FT STRAND 168 168
FT TURN 179 179
FT STRAND 190 190
FT STRAND 192 192
FT HELIX 195 195
FT TURN 202 202
FT STRAND 205 205
FT STRAND 212 212
FT TURN 215 215
FT TURN 227 227
FT STRAND 226 226
FT TURN 240 240
FT HELIX 243 243
FT STRAND 264 264
FT TURN 268 268
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FT HELIX 275 275
FT TURN 277 277
FT HELIX 289 289
FT STRAND 294 294
FT STRAND 304 304
FT TURN 314 314
FT HELIX 316 316
FT STRAND 323 323
FT HELIX 335 335
FT TURN 337 337
FT HELIX 341 341
FT TURN 344 344
FT HELIX 347 347
FT HELIX 352 352
FT HELIX 354 354
FT STRAND 357 357
FT TURN 364 364
Calcium 2.
Calcium 1 (via carbonyl oxygen).
Calcium 3 (via carbonyl oxygen).
Calcium 3 (via carbonyl oxygen).
Calcium 3 (via carbonyl oxygen).
Calcium 3.
Calcium 3.
Calcium 3.
M -> V (in Ref. 3).
L -> W (in Ref. 3).
L -> S (in Ref. 2 and 3).
P -> H (in Ref. 2 and 3).
A -> T (in Ref. 2 and 5).
T -> I (in Ref. 4).
P -> N (in Ref. 3).
S -> N (in Ref. 2, 3 and 4).
TNI -> RTU (in Ref. 4).
D -> Y (in Ref. 2, 3 and 4).
M -> T (in Ref. 2 and 3).
T -> A (in Ref. 2 and 3).
R -> S (in Ref. 3).
T -> N (in Ref. 3).
V -> C (in Ref. 2 and 3).
WS -> RP (in Ref. 2).
S -> P (in Ref. 2).
D -> G (in Ref. 2 and 3).


```

FT TURN 368 369
FT TURN 371 372
FT TURN 378 380
FT HELIX 381 390
FT STRAND 395 399
FT HELIX 400 404
FT STRAND 406 406
FT HELIX 407 409
FT TURN 410 410
FT STRAND 411 411
FT HELIX 415 427
FT TURN 428 428
FT STRAND 433 436
FT STRAND 442 447
FT STRAND 450 450
FT TURN 451 452
FT STRAND 453 453
FT TURN 454 455
FT STRAND 458 463
FT STRAND 468 473
FT HELIX 476 478
FT TURN 479 480
FT STRAND 482 485
FT TURN 486 487
FT STRAND 493 495
FT TURN 498 499
FT STRAND 501 506

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Query Match 66.7%; Score 1908.5; DB 1; Length 549;
 Best Local Similarity 65.6%; Pred. No. 1.6e-120;
 Matches 339; Conservative 75; Mismatches 98; Indels 5; Gaps 3;

```

QY 1 MTLNRRIIS---VLTLLAAVAVLPYMTBPAQAHNGTNGTMQYFPMHLNDGNHNR 57
DB 1 MTLNRRIIS---VLTLLAAVAVLPYMTBPAQAHNGTNGTMQYFPMHLNDGNHNR 59
QY 58 LRDDAANKSKGITAIVIPPAWKGTQNDVGYGAYDLYDLGFEFNOGKTVRTKYGTSOLO 117
DB 60 VANEANNLSIGITLMLPRPAVKGTSRSDVGYGVYDLYDLGFEFNOGKAVRTKYGTKAYL 119
QY 118 GAVTSLKNGGIGQYGVGVVNMHKGADGTEMVNAVEVNSNRNOISGEYTIEMTKFDP 177
DB 120 QAIQAAHAAGQYVADVVPFDHKGADGTEWDAVEVNSDRNOISGTYQIQAMTKFDP 179
QY 178 GRGNTHSFKRWYHFDGTDMDQSOLOKTIYKFGCTGKAMDWEVDINGVYDLYMADI 237
DB 180 GRGNTHSFKRWYHFDGTDMDQSOLOKTIYKFGCTGKAMDWEVDINGVYDLYMADI 238
QY 238 DMDHEVINELRNMGVMTNTLTNLDPRIIDAVKHKYSYTRDMLTHVNTTGKMPFAVAE 297
DB 239 DMDHEVINELRNMGVMTNTLTNLDPRIIDAVKHKYSYTRDMLTHVNTTGKMPFAVAE 298
QY 298 FWKDILAENYLNKTSWNHVSFVDFPLHYNLNYSNSGSGYFDMRNILNGSVVQKPIHAV 357
DB 299 YMSYDINKLHNYIKMTNGTMSLFDAPLNKFTASKSGTGTDMRTLMNTLMKQPTLAV 358
QY 358 TFWVNDHDSQBEALBSFQSWFKPLAYALLITRECGYSVRYGDIYGIPTGVPSMSKI 417
DB 359 TFWVNDHDSQBEALBSFQSWFKPLAYALLITRECGYSVRYGDIYGIPTGVPSMSKI 418
QY 418 DPLLOAROTYAVGTQHDYFDHDDIIGWTRREGSSHPNSGLATIMSDGFGKMMYVVGAK 477
DB 419 DPLLOAROTYAVGTQHDYFDHDDIIGWTRREGSSHPNSGLATIMSDGFGKMMYVVGAK 478
QY 478 AGQVWRDITGNRSGTITINADGMGNTFYNGAVSVWV 514
DB 479 AGQVWRDITGNRSGTITINADGMGNTFYNGAVSVWV 515

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RESULT 15
 ID Q93148
 AC Q93148; PRELIMINARY; PRT; 501 AA.

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DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Amylase.
GN Name=amyK38;
OS Bacillus sp. KSM-K38.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxId=129736;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=KSM-K38;
RX MEDLINE=21347468; PubMed=11453991;
RA Hagihara H., Hayashi Y., Endo K., Igaraeishi K., Ozawa T., Kawai S.,
RA Ozaki K., Ito S.;
RT "deduced amino-acid sequence of a calcium-free alpha-amylase from a
RT strain of Bacillus: implications from molecular modeling of high
RT oxidation stability and chelator resistance of the enzyme.";
RL Eur. J. Biochem. 268:3974-3982(2001).
DR EMBL, AB051102; BAB71820.1; -.
DR PDB, 1UD2; X-ray; A=22-501.
DR PDB, 1UD3; X-ray; A=22-501.
DR PDB, 1UD4; X-ray; A=22-501.
DR PDB, 1UD5; X-ray; A=22-501.
DR PDB, 1UD6; X-ray; A=22-501.
DR PDB, 1UD8; X-ray; A=22-501.
DR GO: 0004556; F:alpha-amylase activity; IEA.
DR GO: 0005975; P:carbohydrate metabolism; IEA.
DR InterPro: IPR006047; Alpha-amylase; 1.
DR Pfam: PF00128; Alpha-amylase; 1.
SQ SEQUENCE 501 AA; 57485 MW; 1240F46739A5C11 CRC64;

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Query Match 65.2%; Score 1866; DB 2; Length 501;
 Best Local Similarity 65.5%; Pred. No. 1e-117;
 Matches 329; Conservative 67; Mismatches 98; Indels 8; Gaps 3;

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QY 15 LLAVALPFPYMTBPAQAHNGTNGTMQYFPMHLNDGNHNRRLDDAANKSKGITAIV 74
DB 8 MLAVLPFPYSVVA-----DGLNGTMQYFPMHLNDGNHNRRLDDAANKSKGITAIV 62
QY 75 IPPAWKGTQNDVGYGAYDLYDLGFEFNOGKTVRTKYGTSOLOQAVTSLKNGGIGQYGV 134
DB 63 IPPAWKGTQNDVGYGAYDLYDLGFEFNOGKTVRTKYGTSOLOQAVTSLKNGGIGQYGV 122
QY 135 VNMHKGADGTEMVNAVEVNSNRNOISGEYTIEMTKFDPGRGNTHSFKRWYHFD 194
DB 123 VNMHKGADGTEMVNAVEVNSNRNOISGEYTIEMTKFDPGRGNTHSFKRWYHFD 182
QY 195 GTMDQSOLOKTIYKFGCTGKAMDWEVDINGVYDLYMADI 254
DB 183 GTMDQSOLOKTIYKFGCTGKAMDWEVDINGVYDLYMADI 239
QY 255 YTNLTNLDPRIIDAVKHKYSYTRDMLTHVNTTGKMPFAVAE 314
DB 240 YTNLTNLDPRIIDAVKHKYSYTRDMLTHVNTTGKMPFAVAE 314
QY 315 WNSHVSFVDFPLHYNLNYSNSGSGYFDMRNILNGSVVQKPIHAVTVDNHDSQBEALBSF 374
DB 300 WNSHVSFVDFPLHYNLNYSNSGSGYFDMRNILNGSVVQKPIHAVTVDNHDSQBEALBSF 359
QY 375 VQSWFKPLAYALLITRECGYSVRYGDIYGIPTGVPSMSKI 434
DB 360 VQSWFKPLAYALLITRECGYSVRYGDIYGIPTGVPSMSKI 419
QY 435 YFDHDDIIGWTRREGSSHPNSGLATIMSDGFGKMMYVVGAK 494
DB 420 YFDHDDIIGWTRREGSSHPNSGLATIMSDGFGKMMYVVGAK 479
QY 495 INADGMGNTFYNGAVSVWV 516
DB 480 INADGMGNTFYNGAVSVWV 501

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Thu May 5 18:22:56 2005

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Job time : 78 secs

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